

STIC-Biotech/ChemLib

71313

From: Salimi, Ali  
Sent: Thursday, July 18, 2002 2:28 PM  
To: STIC-Biotech/ChemLib  
Subject: 09/514,245

Can you please conduct a search and interference for the application serial no. 09/514,245:

SEQ ID NO: 25

Thanks!

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AU 1648  
Room 9D07  
Mailbox 8E12

Point of Contact:  
Susan Hanley  
Technical Info. Specialist  
CM1 6B05 Tel: 305-4053

CRFE

Searcher: \_\_\_\_\_  
Phone: \_\_\_\_\_  
Location: \_\_\_\_\_  
Date Picked Up: \_\_\_\_\_  
Date Completed: \_\_\_\_\_  
Searcher Prep/Review: \_\_\_\_\_  
Clerical: \_\_\_\_\_  
Online time: \_\_\_\_\_

TYPE OF SEARCH:  
NA Sequences: \_\_\_\_\_  
AA Sequences: \_\_\_\_\_  
Structures: \_\_\_\_\_  
Bibliographic: \_\_\_\_\_  
Litigation: \_\_\_\_\_  
Full text: \_\_\_\_\_  
Patent Family: \_\_\_\_\_  
Other: \_\_\_\_\_

VENDOR/COST (where applic.)  
STN: \_\_\_\_\_  
DIALOG: \_\_\_\_\_  
Questel/Orbit: \_\_\_\_\_  
DRLink: \_\_\_\_\_  
Lexis/Nexis: \_\_\_\_\_  
Sequence Sys.: \_\_\_\_\_  
WWW/Internet: \_\_\_\_\_  
Other (specify): \_\_\_\_\_

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 23, 2002, 07:37:49 ; Search time 1857.76 Seconds  
(without alignments)  
7907.603 Million cell updates/sec

Title: US-09-514-245B-25  
Perfect score: 702  
Sequence: 1 atgacgtatcaaggaggcg.....acccccacttaacccttaa 702

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues  
Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : GenEmbl.\*

- 1: gb\_ba.\*
- 2: gb\_hgt.\*
- 3: gb\_in.\*
- 4: gb\_om.\*
- 5: gb\_ov.\*
- 6: gb\_pat.\*
- 7: gb\_ph.\*
- 8: gb\_pl.\*
- 9: gb\_pr.\*
- 10: gb\_ro.\*
- 11: gb\_sts.\*
- 12: gb\_sy.\*
- 13: gb\_un.\*
- 14: gb\_vi.\*
- 15: em\_ba.\*
- 16: em\_fun.\*
- 17: em\_hum.\*
- 18: em\_in.\*
- 19: em\_mu.\*
- 20: em\_om.\*
- 21: em\_or.\*
- 22: em\_ov.\*
- 23: em\_pat.\*
- 24: em\_ph.\*
- 25: em\_pl.\*
- 26: em\_ro.\*
- 27: em\_sts.\*
- 28: em\_un.\*
- 29: em\_vi.\*
- 30: em\_htg\_hum.\*
- 31: em\_htg\_inv.\*
- 32: em\_htg\_other.\*
- 33: em\_htgo\_inv.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
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RESULT	1	AX003277	AX003277	Sequence 12 from Patent WO9929871.	702 bp	DNA	linear	PAT 24-AUG-2000
LOCUS	AX003277	AX003277	AX003277	Sequence 12 from Patent WO9929871.	702 bp	DNA	linear	PAT 24-AUG-2000
DEFINITION	AX003277	AX003277	AX003277	Sequence 12 from Patent WO9929871.	702 bp	DNA	linear	PAT 24-AUG-2000
ACCESSION	AX003277	AX003277	AX003277	Sequence 12 from Patent WO9929871.	702 bp	DNA	linear	PAT 24-AUG-2000
VERSION	AX003277.1	GI:9927101	GI:9927101	Sequence 12 from Patent WO9929871.	702 bp	DNA	linear	PAT 24-AUG-2000
KEYWORDS	AX003277.1	GI:9927101	GI:9927101	Sequence 12 from Patent WO9929871.	702 bp	DNA	linear	PAT 24-AUG-2000
SOURCE	AX003277.1	GI:9927101	GI:9927101	Sequence 12 from Patent WO9929871.	702 bp	DNA	linear	PAT 24-AUG-2000
ORGANISM	AX003277.1	GI:9927101	GI:9927101	Sequence 12 from Patent WO9929871.	702 bp	DNA	linear	PAT 24-AUG-2000
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AUTHORS	AX003277.1	GI:9927101	GI:9927101	Sequence 12 from Patent WO9929871.	702 bp	DNA	linear	PAT 24-AUG-2000
TITLE	AX003277.1	GI:9927101	GI:9927101	Sequence 12 from Patent WO9929871.	702 bp	DNA	linear	PAT 24-AUG-2000
JOURNAL	AX003277.1	GI:9927101	GI:9927101	Sequence 12 from Patent WO9929871.	702 bp	DNA	linear	PAT 24-AUG-2000
FEATURES	AX003277.1	GI:9927101	GI:9927101	Sequence 12 from Patent WO9929871.	702 bp	DNA	linear	PAT 24-AUG-2000
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1. 702	AX003277.1	GI:9927101	GI:9927101	Sequence 12 from Patent WO9929871.	702 bp	DNA	linear	PAT 24-AUG-2000
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ORIGIN	AX003277.1	GI:9927101	GI:9927101	Sequence 12 from Patent WO9929871.	702 bp	DNA	linear	PAT 24-AUG-2000

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ORIGIN																							
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Best Local Similarity		100.0%;		Pred. No. 3.2e-189;																			
Matches 702;		Conservative 0;		Mismatches 0;		Indels 0;		Gaps 0;															
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Db	1734	ATGAGGTATCCAAGGAGCGGTACCGAAGAAGAAGACACCGCCCGCAGCCATCTTGGC	1675																				
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Db	1674	CAGATCTCCGCGCGCGCCCTGGCTGTCCACCCCGCCACCGTTACCGCTGGAGAAG	1615																				
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Db	1614	AAAATGGCATCTTCAACACCGCGCTCTCCCGCACCTTCGGGATATACTGTCAAGCGAAC	1555																				
Qy	181	acagtcagaacgcctctctggcggtgacatgatgagattcaattaatgactttctt	240																				
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Db	1434	GTTAAGGTTGAATTTCTGGCCCTGTCCCGCGATCACCCAGGTGACAGGGGAGTGGGCTCC	1375																				
Qy	361	agtgctgttattttagatgaactttgttaacaaaggccacagccctcaccatgacccc	420																				
Db	1374	AGTGTGTTATTTTAGATGAATACTTTGTAAAGAGCCACAGCCCTCACCTATGACCCC	1315																				
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RESULT 3																							
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LOCUS		AX003275						PAT 24-AUG-2000															
DEFINITION		porcine circovirus.																					
ACCESSION		AX003275																					
VERSION		AX003275.1 GI:9927099																					
KEYWORDS		. porcine circovirus.																					
SOURCE		ORGANISM																					
REFERENCE		Viruses; ssDNA viruses; Circoviridae; Circovirus.																					
AUTHORS		Hutet,E. and Albina,E.																					
TITLE		Circovirus sequences related to piglet weight loss disease (pwd)																					
JOURNAL		HUTET EVELYNE (FR); ALBINA EMMANUEL (FR)																					
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FEATURES source Location/Qualifiers  
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Query Match 100.0%; Score 702; DB 6; Length 1767;  
Best Local Similarity 100.0%; Pred. NO. 3.2e-189;  
Matches 702; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 61 cagatcctccgcgcgcgccttgctctccacccccgcacggtaccgctggagaag 120  
Db 94 CAGATCCTCCGCGCGCGCTCGCTCGTCCACCGCCGCGACCGTTACCGCTGGAGAAG 153  
Qy 121 aaaaatggcatctcaacacccgctctcccgaccctcgatatactgtcaagcgaacc 180  
Db 154 AAAATGGCATCTTCAACACCCGCCCTCTCCCGCACCTTCGGATATACTGTCAACGGAAC 213  
Qy 181 acagtccagaacgcctcctcgggcggtggacatgatgagattcaatataatgactttctt 240  
Db 214 ACAGTCAGAACGCCCTCTCGGCGGTGGACATGATGAGATTCATATTAATGACTTTCTT 273  
Qy 241 cccccgggggggggtcaaacccccgcgctctgtgccctttgaatactactagaataaag 300  
Db 274 CCCCCAGGAGGGGGTCAAAACCCCGCTCTGTGCCCTTTGAATACTACAGAAATAAGAAAG 333  
Qy 301 gtaaggtgaattctggcctctcccgatcacccaggtgacagggagtggtctcc 360  
Db 334 GTTAAGGTTGAATCTGGCCCTCTCCCGCATCACCAGGGTGACAGGGAGTGGGCTCC 393  
Qy 361 agtgcgttatatttagatgataactttgtaacaaagccacagccctcacctatgacccc 420  
Db 394 AGTGCCTGTTATTTAGATGATACTTTGTAAACAAAGCCACAGCCCTCACCATTGACCCC 453  
Qy 421 tatgtaaactactctccgcgcataccataacccagccctctctctaccactcccggtac 480  
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Qy 481 ttatcccccacacgtctctagatttcaactattgattacttcaacccaacacaaaga 540  
Db 514 TTACCCCCAAACCTCTCTAGATTTTCACTATTGATTACTTCCAAACCAACAAACAAAGA 573  
Qy 541 aaccagctggtgagactacaaaactgctggaatgtagaccagtaggcctcgccact 600  
Db 574 ACCAGCTGTGGCTGAGACTACAAACTGCTGGAATGTAGACACAGTAGGCGCTCGGCACT 633  
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Db 634 CGCTTCGAAACAGTATATAGCACCAGGAATACAATATCCGTGTGTAACCATGTATGTACA 693  
Qy 661 ttcagagaatttaattttaagaccctcccccacttaacccctaa 702  
Db 694 TTCAGAGAATTTAAATTTAAAGACCCGCCCACTTAACCCCTTAA 735

RESULT 4  
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DEFINITION Porcine circovirus type 2 isolate FRA3, complete genome.  
ACCESSION AF201311  
VERSION AF201311.1 GI:7021361  
KEYWORDS porcine circovirus type 2.  
SOURCE porcine circovirus type 2.  
ORGANISM Viruses; ssDNA viruses; Circoviridae; Circovirus.  
REFERENCE 1 (bases 1 to 1767)

AUTHORS Mankertz,A., Domingo,M., Folch,J.M., LeCann,P., Jestin,A., Segales,J., Chmielewicz,B., Plana-Duran,J. and Soike,D.  
TITLE Characterisation of pcv-2 isolates from Spain, Germany and France  
JOURNAL Virus Res. 66 (1), 65-77 (2000)  
MEDLINE 20120936  
REFERENCE 2 (bases 1 to 1767)  
AUTHORS Mankertz,A., Domingo,M., Folch,J.M., LeCann,P., Jestin,A., Segales,J., Chmielewicz,B., Plana-Duran,J. and Soike,D.  
TITLE Direct Submission  
JOURNAL Submitted (03-NOV-1999) P24, Robert Koch Institut, Nordufer 20, Berlin 13353, Germany  
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Db 617 AAAAATGGCATCTTCAACACCGCCTCTCCCGCACCTTCGGATATACTGTCAAGGAAC 558  
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Db 497 CCCCCAGGAGGGGCTCAACACCCCGCTCTGTGCCCTTTGAATACTACAGATAGAAAG 438

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AF201897			
ACCESSION			
AF201897.1			
VERSION			
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SOURCE			
ORGANISM			
1 (bases 1 to 1767)			
REFERENCE			
AUTHORS			
Wellenberg,G.J., Pesch,S., Berendsen,F.W., Steverink,P.J.G.M.,			
Hunneberg,W., Van der Vorst,J.K., Peperkamp,N.H.M.T.,			
Ohlinger,V.F., Schippers,R., Van Oirschot,J.T. and de Jong,M.F.			
Isolation and characterization of porcine circovirus type 2 from			
pigs showing signs of post-weaning multisystemic wasting syndrome			
in The Netherlands			
Unpublished			
JOURNAL			
REFERENCE			
AUTHORS			
Pesch,S. and Ohlinger,V.F.			
TITLE			
Submitted (04-NOV-1999); Virology and Molecular Epidemiology,			
Bioscreen European Veterinary Disease Management Center GmbH, 11			
Mendelstr., Muenster, NRW 48149, Germany			
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Db	1682	CAGATCCTCCGGCGCGCCCTGGCTCGTCCACCCCGCCACCGTTACCGCTGGAGAAG	1623		
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Db	1622	AAAATGGCATCTTCAACACCCGCCCTCTCCGCGACCTTCGGATATACTATCAACGGAACC	1563		
Qy	181	acagtcagaacccctcctctgggcggtggacatgatgagattcaatattaatgactttctt	240		
Db	1562	ACAGTCAAGACGCCCTCCCTGGGGGGTGGACATGATGAGATTCAATATTAATGACTTCTT	1503		
Qy	241	ccccagaggggggttcaaacccccgcctctgtcccttttgaatactacagaataagaag	300		
Db	1502	CCCCCAGGAGGGGGCTCAAAACCCCGCTCTGTGCCCTTTGAATACTACAGAATAAGAAAG	1443		
Qy	301	gtaagttgaaattcttggccctctcccgatcacccagagtgacagggagtgggctcc	360		
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Qy	361	agtctgttatttagatgataactttgtaacaaaggccacagccctcaactatgaacccc	420		
Db	1382	AGTGTGTTATTCTAGATGATACTTTGTAAACAAAGSCCAGACGCCCTCACCTATGACCCC	1323		
Qy	421	tatgtaaaactactcctccgcgcataacataaccagcccttctcctaccactccgggtac	480		
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Qy	481	tttaccaccaaacctctctagatttcactattgattacttcaactcaacaaacacaaaga	540		
Db	1262	TTTACCCCAAAACCTGCTCTAGATTCCACTATTGATTACTTCCAACCAACAAACAAAGA	1203		
Qy	541	aaccagctggctgagactacaaactgctggaatgtagacacagtagcgctcgacct	600		
Db	1202	AATCAGCTGCTGGCTGAGACTACAAGCTGCTGGAATGTACACACCTAGGCTCGGCAC	1143		
Qy	601	gcgttgaaaaacagtatatcacgaccagggaatacaataatccgtgttaaccatgtatgtacaa	660		
Db	1142	GGGTTGGAACACAGTATATACGACCGAGGAATAAATATCGTGTAAACCATGTATGTACAA	1083		
Qy	661	ttcagagaatttaatttaagaccccccaacttaaccccttaa	702		
Db	1082	TTCAGAGAATTTAATCTTAAGACCCCCCCTTAACCCCTTAA	1041		
RESULT	7				
LOCUS	AY035820/c	AY035820	1767 bp	DNA	circular VRL 13-JUN-2001
DEFINITION	Porcine circovirus type 2, complete genome.				
ACCESSION	AY035820				
VERSION	AY035820.1 GI:14422165				
KEYWORDS	porcine circovirus type 2.				
SOURCE	porcine circovirus type 2.				
REFERENCE	1 (bases 1 to 1767)				
AUTHORS	Shengbo, C. and Huanchun, C.				
TITLE	Cloning and sequence analysis of the genome of Porcine Circovirus				
JOURNAL	type 2 isolated from pig with PMWS in China				
REFERENCE	2 (bases 1 to 1767)				
AUTHORS	Shengbo C. and Huanchun, C.				
TITLE	Direct Submission				
JOURNAL	Submitted (16-MAY-2001) Animal Medicine, Hua Zhong Agricultural				
FEATURES	University, Shi Zi Shan, Wuhan, Hubei 430070, P. R. China				
source	Location/Qualifiers				
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51..995					
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816..824					
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1016..1105					
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BASE COUNT      456 a   358 c   500 g   454 t
ORIGIN

Query Match      89.3%; Score 626.8; DB 14; Length 1768;
Best Local Similarity 93.3%; Pred. No. 9.1e-168;
Matches 655; Conservative 0; Mismatches 47; Indels 0; Gaps 0;

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QY 61 cagatcctccgcgcgcgccttgctgcgtccacccccgcgcacgctaccgctgcgaag 120
DB 678 CAGATCTCCGCCCGCCCTGGCTGCTGCACCCCGCCACCGCTTACCGCTGGAGAAG 619

QY 121 aaaaatggcatcttcaacacccgcctctccgcgcacctcgatatactgtcaacgcgaac 180
DB 618 AAAAAATGGCATCTTCAACACCCGGCTCTCCCGCACCTTCGGATATCTGTCAAGGCTACC 559

QY 181 acagtcagaacgcctcctctggcggtggacatgatgagattcaataataatgactttctt 240
DB 558 ACAGTCAGACCGCCTCTCTGGCGGTGCACATGATGAGATTTAATATTGACGACTTTGTT 499

QY 241 cccccagaggggggtcaaaacccccgcctctgtgcccccttgaataactacagaataaaga 300
DB 498 CCCCCGAGGGGGGACCAAAAATCTCTATACCCCTTTGAATATTACTAGAAATAGAAG 439

QY 301 gtaagctgaattctggccctgcctcccgatcacccagggatgacagggagtgagctcc 360
DB 438 GTTAAGGTTGAATTTCTGGCCCTGTCTCCCAATACCCAGGGGTATAGGGAGTGGGTCC 379

QY 361 agtgcgttatatttagatgataaactttgtcaaaagggcacagccctcacctatgacccc 420
DB 378 ACTGCTGTTATTCTAGATGATACTTTGTACAAGGCCACAGCCCTTAACCTATGACCCC 319

QY 421 tatgtaactactcctcccgccataaccataccagcccttctcctaccactcccggtac 480
DB 318 TATGTAAACTACTCCTCCGCGCATACAATCCCCACCCCTTCTCTACCACCTCCCGGTAC 259

QY 481 ttaccaccccaaacctgctctagatttccactattgattacttccaaacaaacaaacaaga 540
DB 258 TTTACCCCCCAAAACCTGTCTTGTATTTCACCTATTGATTACTTCCAACCAATAACAAAAG 199

QY 541 aaccagctgtggctgagactacaaactgctggaataatgagaccagtaggcctcgacct 600
DB 198 ANTACAGCTTTGGCTGAGGCTACAAAACCTCTGCAAAATGTGGACACAGTAGGCTCGGCAC 139

QY 601 gcgttcgaaaacagtatatacagaccaggaatacaaatccggtgtaaaccatgtatgtacaa 660
DB 138 GCCTTCGAAAACAGTAAATACGACCAGGACTTACAATATCCGTGTAAACCATGTATGTACAA 79

QY 661 ttcagagaatttaattttaagaaccccccaacttaaccccttaa 702
DB 78 TTCAGAGAATTTAATCTTTAAAGACGCCCCCCTTTAAACCCCTAA 37

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RESULT	9
LOCUS	AF086835/c
DEFINITION	Porcine circovirus strain 9741, complete genome.
ACCESSION	AF086835
VERSION	AF086835.1 GI:3661518
KEYWORDS	.
SOURCE	porcine circovirus.
ORGANISM	porcine circovirus.

Viruses; ssDNA viruses; Circoviridae; Circovirus.  
1 (bases 1 to 1768)  
Wang,L., Willson,P., Chow,B., Gibbons,E. and Babiuk,L.  
Emergence of a new porcine circovirus  
Unpublished  
2 (bases 1 to 1768)  
Wang,L., Willson,P., Chow,B., Gibbons,E. and Babiuk,L.  
Direct Submission  
Submitted (26-AUG-1998) VIDO, University of Saskatchewan, 120  
Veterinary Road, Saskatoon, Saskatchewan S7N 5E3, Canada  
Location/Qualifiers  
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ORIGIN

Query Match 88.8%; Score 623.6; DB 14; Length 1768;  
Best Local Similarity 93.0%; Pred. No. 7.4e-167;  
Matches 653; Conservative 0; Mismatches 49; Indels 0; Gaps 0;

QY 1 atacgtatccaaggagcgttacccaagaagaagacaccccccagccatcttggc 60  
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Db 1735 ATGACGTATCAAGAGGCGGTACCGCAGAAGAAGACACCCCGCCGACCATCTTGGC 1676  
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QY 61 cagatctccgcgcgcgccttgctgcgtccaccccccacgcgttaccgctggagaag 120  
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Db 1675 CAGATCTCCGCGCGCCCTCGTCTGCTCCACCCCGCACCGCTACCGTTGAGAAG 1616  
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QY 121 aaaaatggcatcttcaacacccgcctctccgcaccttcggatatactgtcaagcgaa 180  
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Db 1615 AAAAATGGCATCTTCAACACCCGCGCTCTCCGCGACCTTCGGATATACTGTCAAGCGTACC 1556  
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QY 181 acagtcaaacgcctcctggcggtgacatgatgattcaataatgatcttctt 240  
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Db 1555 ACAGTCACACGCCCTCCTGGCGGTGGACATGATGAGATTTAAATGACGACTTTGTT 1496  
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QY 241 cccccaggagggggtcaaaccccccctctgtgcctttgaatactactacagaataagaag 300  
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Db 1435 GTTAAGGTTGAATTTCTGGCCTGTCTCCCCCATCACCCAGGGTGATAGGGAGTGGGCTCC 1376  
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QY 361 agtgccttattttaagtataactttgtacaagaagccacagccctcacctatgacccc 420  
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Db 1375 ACTGCTGTTATTTAGATGATAACTTTGTAAACAAAGGCCACAGCCCTTAACCTATGACCCA 1316  
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QY 421 tatgtaaactactcctcccgcctataccataagccagcccttctctaccactcccgatc 480  
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Db	1315		TATGTAACACTCTCCCGCCATACAAATCCCAACCCCTTCCTACCACTCCCGTTAC	1256
Qy	481		tttaccocccaaacctgctctagattccactattgattacttccaaacacaaacaaaga	540
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Qy	601		gggttcgaaacagtatatacagcagggaatacaaatatccgttaaccatgtatgtacaa	660
Db	1135		GGGTTGGAACACAGTAATAACGACCGAGGACTACAATAATCCGTGAACCATGTATGACAA	1076
Qy	661		tccagagaatttaatttaagaacccccccacttaaaccttaa	702
Db	1075		TTCAGAGATTTAATCTTAAGACCCCCCACCTTAACCCCTAA	1034
RESULT	10			
LOCUS	AF109398/c		1768 bp	DNA circular VRL 23-JUL-2001
DEFINITION	Porcine circovirus type 2-C, complete genome.			
ACCESSION	AF109398			
VERSION	AF109398.1	GI:4106885		
KEYWORDS	porcine circovirus type 2-C.			
SOURCE	porcine circovirus type 2-C.			
ORGANISM	Viruses; ssDNA viruses; Circoviridae; Circovirus.			
REFERENCE	1 (bases 1 to 1768)			
AUTHORS	Hamel,A.L., Lin,L.L., Sachvie,C., Grudeski,E. and Nayar,G.P.S.			
TITLE	PCR detection and characterization of type-2 porcine circovirus			
JOURNAL	Can. J. Vet. Res. 64 (1), 44-52 (2000)			
MEDLINE	20142849			
PUBMED	10680656			
REFERENCE	2 (bases 1 to 1768)			
AUTHORS	Hamel,A.L. and Nayar,G.P.S.			
TITLE	Nucleotide sequence of four different isolates of circovirus			
JOURNAL	Unpublished			
REFERENCE	3 (bases 1 to 1768)			
AUTHORS	Hamel,A.L. and Nayar,G.P.S.			
TITLE	Direct Submission			
JOURNAL	Submitted (27-NOV-1998) Virology Laboratory, Veterinary Diagnostic Laboratory, Manitoba Agriculture, 545 University Crescent, Winnipeg, Manitoba R3T 5S6, Canada			
FEATURES	Location/Qualifiers			
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CDS	1016. .1177			
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DEFINITION Porcine circovirus complete genome.
ACCESSION AF166528
VERSION AF166528.1 GI:5739338
KEYWORDS porcine circovirus.
SOURCE porcine circovirus.
ORGANISM Viruses; ssDNA viruses; Circoviridae; Circovirus.
REFERENCE 1 (bases 1 to 1768)
AUTHORS Yang, K.H., Lee, Y.F., Chao, D.S., Shieh, Y.C. and Lai, S.S.
TITLE Complete nucleotide sequences of porcine circovirus Tainan strand outbreak in Taiwan
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1768)
AUTHORS Yang, K.H., Lee, Y.F., Chao, D.S., Shieh, Y.C. and Lai, S.S.
TITLE Direct Submission
JOURNAL Submitted (08-JUL-1999) Veterinary Medicine, National Chia-Yi Institute of Technology, 300 Shei Fu Road, Lu Liao Li, Chia-Yi City 600, Taiwan
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BASE COUNT 453 a 367 c 492 g 456 t
ORIGIN

Query Match 88.8%; Score 623.6; DB 14; Length 1768;
Best Local Similarity 93.0%; Pred. No. 7.4e-167;
Matches 653; Conservative 0; Mismatches 49; Indels 0; Gaps 0;

QY 1 atgacgtatccaaggaggcttaccgaagaagacacgcccccgagccattctggc 60
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Db 1735 ATCAGCATCAAGAGGCGCTTCCGAGAGAGACACGCGCCCGCAGCATCTTGGC 1676
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QY 61 cagatctccgcgcgcgccttgctcgctccacccccgcacccgttacccgtgagaag 120
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Db 1675 CAGATCTCGCGCGCGCGCCCTGGCTCGTCCACCCCGCACCGTTACCGCTGGAGAAG 1616
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Db 1555 ACAGTCAGAACGCCCTCTCGCGGTGGACATGATGAGATTTAATATTAAACGACTTTGTT 1496
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Db 1495 CCCCCGGAGGGGGGACCAAAATCTCTATACCTTTGAATCTACTACAGAAATAAGAAAG 1436
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QY 301 gttaaaggttgaaattcttggccctgctccccgatcaccacgggtgacaggggagtgctcc 360
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QY 601 gcgttcgaaaaacagtatatacgaccaggaaatcacaaatcccggtgaaccatgtatgtacaa 660
Db 1135 GCGTTCGAAAACAGTAAATAGCACCAGGACTACAAATATCCGTGTAAACCATGTATGTACAA 1076
QY 661 ttcagagaatttaattttaagacccccccacttaacccttaa 702
Db 1075 TTCAGAGAATTAAATCTTAAAGACCCCCCACTTAAACCCCTAA 1034
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Search completed: July 23, 2002, 09:55:49  
Job time: 8280 sec

Result No.	Query			ID	Description
	Score	Match	Length		
C 1	381.6	54.4	1767	4	US-09-347-594-1
C 2	378.4	53.9	1767	4	US-09-347-594-2
C 3	340	48.4	1768	4	US-09-347-594-3
C 4	340	48.4	1768	4	US-09-347-594-4
C 5	307.8	43.8	699	4	US-09-267-177-24
C 6	307.8	43.8	1727	4	US-09-267-177-2
C 7	307.8	43.8	1759	4	US-09-267-177-38
C 8	307.8	43.8	1759	4	US-09-267-177-40
C 9	303.2	43.2	687	4	US-09-267-177-25
C 10	299	42.6	1674	4	US-09-267-177-1
C 11	199.4	28.4	1759	4	US-09-347-594-5
C 12	172.2	24.5	285	4	US-09-267-177-22
C 13	44.6	6.4	4403765	4	US-09-103-840A-2
C 14	41.8	6.0	322	4	US-09-117-121-41
C 15	41.8	6.0	9997	1	US-08-246-982A-15
C 16	41.8	6.0	9997	1	US-08-453-265-15
C 17	41.8	6.0	10103	2	US-08-457-273B-7
C 18	41.8	6.0	10348	2	US-08-457-273B-41
C 19	41.8	6.0	10348	3	US-08-556-419-13
C 20	41.8	6.0	10348	4	US-09-041-886-14
C 21	41.8	6.0	10366	1	US-08-246-982A-5
C 22	41.8	6.0	10366	1	US-08-453-265-5
C 23	40	5.7	6530	2	US-08-146-930-1
C 24	40	5.7	6530	3	US-08-458-240-1
C 25	40	5.7	6530	5	PCT-US93-03993-1
C 26	39.6	5.6	3000	4	US-08-460-269C-5
C 27	39.4	5.6	1028	4	US-08-118-200-1



Db 1467 TATATACACAGAGAAATACATATCCGTGTAAACCATGTATGTACAAATTCAGAGAAATTTAA 1408  
QY 675 ttttaaagaccccccaacttaacccttaa 702  
Db 1407 TCTTAAAGACCCCCCACTTAACCCCTTAA 1380

## RESULT 2

US-09-347-594-2/c  
; Sequence 2, Application US/09347594

; Patent No. 6217883

; GENERAL INFORMATION:

; APPLICANT: ALLAN, Gordon M.

; APPLICANT: MEEHAN, Brian M.

; APPLICANT: ELLIS, John A.

; APPLICANT: KRAKOWKA, George S.

; APPLICANT: AUDONNET, Jean-Christophe F.

; TITLE OF INVENTION: PORCINE CIRCOVIRUS AND PARVOVIRUS VACCINE

; FILE REFERENCE: 454313-2338

; CURRENT APPLICATION NUMBER: US/09/347,594

; EARLIER FILING DATE: 1999-07-01

; EARLIER APPLICATION NUMBER: 98 08777

; EARLIER FILING DATE: 1998-07-06

; NUMBER OF SEQ ID NOS: 5

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 2

; LENGTH: 1767

; TYPE: DNA

; ORGANISM: Porcine circovirus

US-09-347-594-2

Query Match 53.9%; Score 378.4; DB 4; Length 1767;  
Best Local Similarity 98.5%; Pred. No. 4.6e-108;  
Matches 382; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 315 ctggccctgtccccgataccccaggggtgacaggggagtgaggctccagtgctgtatttt 374  
Db 1767 CTGGCCCTGTCTCCCGATCACCCAGGGTGACAGGGGAGTGGGCTCCAGTGTCTTATTCT 1708  
QY 375 agatgataactttgtacaagggccacagccctcacctatgacccctgtgaaactactc 434  
Db 1707 AGATGATAACTTTGTACAAGGGCCACAGCCCTCACCTATGACCCCTATGTAACACTCTC 1648  
QY 435 ctcccgccataccataaccagccctctctaccactcccggtactttacccccaaacc 494  
Db 1647 CTCCCGCATACCATACCCAGCCCTTCTCTACCACTCCCGCTACTTTACCCCAACC 1588  
QY 495 tgtctagatttcaactattgattacttccaaacaaacaaacaaacaaacagctgtggct 554  
Db 1587 TGTCTAGATTCTCACTATTGATTACTTCCAAACCAACAAACAAAGAAATCAGCTGTGGCT 1528  
QY 555 gagactacaactgtcggaatgtagaccacgttaggcctcggcactcggtcgtaaaacag 614  
Db 1527 GAGACTACAACACTACTCGAAATGTAGACCACGTAGGCTCGGCACCTGCGTTCGAAACAG 1468  
QY 615 tatatagaccaggaatacaataatccgtgtaaccatgtatgataatccagagaatttaa 674  
Db 1467 TATATACGACGAGGAATACAAATATCCGTGTAAACCATGTATGTACAAATTCAGAGAAATTTAA 1408  
QY 675 ttttaaagaccccccaacttaacccttaa 702  
Db 1407 TCTTAAAGACCCCCCACTTAACCCCTTAA 1380

## RESULT 3

US-09-347-594-3/c

; Sequence 3, Application US/09347594

; Patent No. 6217883

; GENERAL INFORMATION:

; APPLICANT: ALLAN, Gordon M.

; APPLICANT: MEEHAN, Brian M.

; APPLICANT: ELLIS, John A.  
; APPLICANT: KRAKOWKA, George S.  
; APPLICANT: AUDONNET, Jean-Christophe F.  
; TITLE OF INVENTION: PORCINE CIRCOVIRUS AND PARVOVIRUS VACCINE  
; FILE REFERENCE: 454313-2338  
; CURRENT APPLICATION NUMBER: US/09/347,594  
; CURRENT FILING DATE: 1999-07-01  
; EARLIER APPLICATION NUMBER: 98 08777  
; EARLIER FILING DATE: 1998-07-06  
; NUMBER OF SEQ ID NOS: 5  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 3  
; LENGTH: 1768  
; TYPE: DNA  
; ORGANISM: Porcine circovirus  
US-09-347-594-3

Query Match 48.4%; Score 340; DB 4; Length 1768;  
Best Local Similarity 92.3%; Pred. No. 4.2e-96;  
Matches 358; Conservative 0; Mismatches 30; Indels 0; Gaps 0;

QY 315 ctggccctgtccccgataccccaggggtgacaggggagtgaggctccagtgctgtatttt 374  
Db 1768 CTGGCCCTGTCTCCCGATCACCCAGGGTGATAGGGGAGTGGGCTCCACCTGCTGTATTCT 1709  
QY 375 agatgataactttgtacaagggccacagccctcacctatgacccctatgtaactactc 434  
Db 1708 AGATGATAACTTTGTACAAGGGCCACAGCCCTTAACCTATGACCCATATGTAACCTACTC 1649  
QY 435 ctcccgccataccataaccagccctctctaccactcccggtactttacccccaaacc 494  
Db 1648 CTCCCGCATACCATACCCCAACCCTTCTCTACCACTCCCGTACTTTCACACCCCAACC 1589  
QY 495 tgtctagatttcaactattgattacttccaaacaaacaaacaaacaaacagctgtggct 554  
Db 1588 TGTCTTAGTCTCACTATTGATTACTTCCAAACCAATAACAAAGAAATCAGCTTTGGCT 1529  
QY 555 gagactacaactgtcggaatgtagaccacgttaggcctcggcactcggtcgtaaaacag 614  
Db 1528 GAGGCTACAACCTCTAGAAATGTGGACCACTAGGCTCGGCACCTGCGTTCGAAACAG 1469  
QY 615 tatatagaccaggaatacaataatccgtgtaaccatgtatgataatccagagaatttaa 674  
Db 1468 TATATACGACGAGGACTACAATATCCGTGTAAACCATGTATGTACAAATTCAGAGAAATTTAA 1409  
QY 675 ttttaaagaccccccaacttaacccttaa 702  
Db 1408 TCTTAAAGACCCCCCACTTTAAACCCCTTAA 1381

## RESULT 4

US-09-347-594-4/c

; Sequence 4, Application US/09347594

; Patent No. 6217883

; GENERAL INFORMATION:

; APPLICANT: ALLAN, Gordon M.

; APPLICANT: MEEHAN, Brian M.

; APPLICANT: ELLIS, John A.

; APPLICANT: KRAKOWKA, George S.

; APPLICANT: AUDONNET, Jean-Christophe F.

; TITLE OF INVENTION: PORCINE CIRCOVIRUS AND PARVOVIRUS VACCINE

; FILE REFERENCE: 454313-2338

; CURRENT APPLICATION NUMBER: US/09/347,594

; EARLIER FILING DATE: 1999-07-01

; EARLIER APPLICATION NUMBER: 98 08777

; EARLIER FILING DATE: 1998-07-06

; NUMBER OF SEQ ID NOS: 5

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 4

; LENGTH: 1768

; TYPE: DNA

; ORGANISM: Porcine circovirus

Db 1651 AACATCTCCGGAGAAAGACCATATTTGGCACACCCCGCTTTCAGAAACCGTTACAGATGG 1592  
QY 115 agaaggaataatgcatcttaacacccgcctctcccgcaacctcggtatatactatgtaag 174  
Db 1591 CGCGAAAGACGGTATCTTCAATTCGCGCTTCTACAGAAATTTGTACTCACCATAAAA 1532  
QY 175 cgaaccagtcgaagacgcctctcggtggagcatgatgagattcaattatgac 234  
Db 1531 GGA---GGATACTCGAGCCATCTTGAATCTTAACCTACCTCAATCAACATCGGCCAG 1475  
QY 235 tttttccccagagaggggggtcaaacccccgcctctgctgccttttgaataactacagaata 294  
Db 1474 TTCTCCCGCTCAGCGGGACCAACCCCTACCCCTACCTTTCATTAATCAATCACTACCGTATT 1415  
QY 295 agaaagttaagtgtaattctgctgcctgcctcccgatcacccaggggtgacagggagtg 354  
Db 1414 AGAAGGCTAAATATGAATTTTACCCAGAGACCCCATCACTCTTAATCAAGAGGTGT 1355  
QY 355 ggtccagtgctgtatttttagatgataaactttgtacaaaggccacagccctccactat 414  
Db 1354 GGGTCCACTGTTTATCTTGGATGCAACTTTGTAAACCCCTCCACCAACTTGGCCTAT 1295  
QY 415 gacctatgtataactactctccgcataccataaacccagcccttctctaccactcc 474  
Db 1294 GACCCCTATATTAACTACTCTCCCGGCACACCATTAAGCGAGCCCTTTACCTACCACTCC 1235  
QY 475 cggtaactttcccccaaacctctcctagatttactattgattacttacttccacaaacaac 534  
Db 1234 AGGTACTTCAACCCCAACCTGAGCTGACCAACAAATTTGTTGGTTCCACCCAAATAT 1175  
QY 535 aaagaacacagctgtggtgagactacaactgctggaatgtagaccagtaggctc 594  
Db 1174 AAAGAAACACGCTGTGCTCCATTTAAATACCCACCAATGTGCGACACACAGGCTC 1115  
QY 595 ggcactgctcgaaacagtatatacagaccaggaatacaatatcgtgtaacatgtat 654  
Db 1114 GGCTATCGCTCCAAAATGACGCACACGCCCAAAATTTATGTTGAAGCTGACTATTAT 1055  
QY 655 gtacaattcagagaatttaatttaagaccccccaactaa 695  
Db 1054 GTACAATTGAGAAATTTATCTCTAAAAGACCCCTCTAAATAA 1014

RESULT 7  
US-09-267-177-38/c  
; Sequence 38, Application US/09267177  
; Patent No. 6287856  
; GENERAL INFORMATION:  
; APPLICANT: Poet, Steven E.  
; APPLICANT: Ritchie, Branson W.  
; APPLICANT: Niagro, Frank D.  
; APPLICANT: Lukert, Phil D.  
; TITLE OF INVENTION: Vaccines against Circovirus Infections  
; FILE REFERENCE: 21099.0057  
; CURRENT APPLICATION NUMBER: US/09/267,177  
; CURRENT FILING DATE: 1999-03-12  
; EARLIER APPLICATION NUMBER: 60/077,890  
; EARLIER FILING DATE: 1998-03-13  
; NUMBER OF SEQ ID NOS: 41  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 38  
; LENGTH: 1759  
; TYPE: DNA  
; ORGANISM: porcine circovirus  
US-09-267-177-38

Query Match 43.8%; Score 307.8; DB 4; Length 1759;  
Best Local Similarity 67.0%; Pred. No. 4.5e-86;  
Matches 470; Conservative 0; Mismatches 22; Indels 9; Gaps 2;  
QY 1 atgacgtatcaagggcggttaccgaagaagacaccccgcccgcatcttggc 60

Db 1723 ATGAGGTGGCCAAAGGAGGGGTTTACCGCAGAAGAGACCGCGCCGAGCCATCTTGA 1664  
QY 61 cagatctccgcgcgcgcgcctctgctgtccaccc-----ccgcacacgttacccgctgg 114  
Db 1663 ACATCTCTCCGAGAAAGACCATATTTGGCACACCCCGCTTTCAGAAACCGTTACAGATGG 1604  
QY 115 agaaggaataatgcatcttcaacacccgcctctcccgacactctcgatatactatgtaag 174  
Db 1603 CGCGAAAGACGGTATCTTCAATTCGCGCTTCTACAGAAATTTGTACTCACCATAAAA 1544  
QY 175 cgaaccagtcgaagacgcctctcggtggagcatgatgagattcaattatgac 234  
Db 1543 GGA---GGATACTCGAGCCATCTTGAATCTTAACCTACCTCAATCAACATCGGCCAG 1487  
QY 235 tttttccccagagaggggggtcaaacccccgcctctgctgccttttgaataactacagaata 294  
Db 1486 TTCTCCCGCTCAGCGGGACCAACCCCTACCCCTACCTTTCATTAATCAATCACTACCGTATT 1427  
QY 295 agaaagttaagtgtaattctgctgcctgcctcccgatcacccaggggtgacagggagtg 354  
Db 1426 AGAAGGCTAAATATGAATTTTACCCAGAGACCCCATCACTCTTAATCAAGAGGTGT 1367  
QY 355 ggtccagtgctgtatttttagatgataaactttgtacaaaggccacagccctccactat 414  
Db 1366 GGGTCCACTGTTTATCTTGGATGCAACTTTGTAAACCCCTCCACCAACTTGGCCTAT 1307  
QY 415 gacctatgtataactactctccgcataccataaacccagcccttctctaccactcc 474  
Db 1306 GACCCCTATATTAACTACTCTCCCGGCACACCATTAAGCGAGCCCTTTACCTACCACTCC 1247  
QY 475 cggtaactttcccccaaacctctcctagatttacttacttccacaaacaac 534  
Db 1246 AGGTACTTCAACCCCAACCTGAGCTGAGCAACAAATTTGTTGGTTCCACCCAAATAT 1187  
QY 535 aaagaacacagctgtggtgagactacaactgctggaatgtagaccagtaggctc 594  
Db 1186 AAAGAAACACGCTGTGCTCCATTTAAATACCCACCAATGTGCGACACACAGGCTC 1127  
QY 595 ggcactgctcgaaacagtatatacagaccaggaatacaatatcgtgtaacatgtat 654  
Db 1126 GGCTATCGCTCCAAAATGACGCACACGCCCAAAATTTATGTTGAAGCTGACTATTAT 1067  
QY 655 gtacaattcagagaatttaatttaagaccccccaactaa 695  
Db 1066 GTACAATTGAGAAATTTATCTCTAAAAGACCCCTCTAAATAA 1026

RESULT 8  
US-09-267-177-40  
; Sequence 40, Application US/09267177  
; Patent No. 6287856  
; GENERAL INFORMATION:  
; APPLICANT: Poet, Steven E.  
; APPLICANT: Ritchie, Branson W.  
; APPLICANT: Niagro, Frank D.  
; APPLICANT: Lukert, Phil D.  
; TITLE OF INVENTION: Vaccines against Circovirus Infections  
; FILE REFERENCE: 21099.0057  
; CURRENT APPLICATION NUMBER: US/09/267,177  
; CURRENT FILING DATE: 1999-03-12  
; EARLIER APPLICATION NUMBER: 60/077,890  
; EARLIER FILING DATE: 1998-03-13  
; NUMBER OF SEQ ID NOS: 41  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 40  
; LENGTH: 1759  
; TYPE: DNA  
; ORGANISM: porcine circovirus  
US-09-267-177-40

Query Match 43.8%; Score 307.8; DB 4; Length 1759;

Qy 115 agaaggaaaatggcat.cttcaacacccgcctctccgcacctcggatatactgtcaag 174

; EARLIER FILING DATE: 1998-03-13  
; NUMBER OF SEQ ID NOS: 41  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 1  
; LENGTH: 1674  
; TYPE: DNA  
; ORGANISM: porcine circovirus  
US-09-267-177-1

Query Match 42.6%; Score 299; DB 4; Length 1674;  
Best Local Similarity 66.8%; Pred. No. 2.4e-83;  
Matches 460; Conservative 0; Mismatches 220; Indels 9; Gaps 2;  
  
QY 13 aggagcggtaccgaagaagaacacccgccccgcagccatcttgccagatctccgc 72  
Db 1674 AGGAGCGGTTACCGCAGACGAAGAGACCGCCCGCGAGCCATCTTGGAAACATCTCCGG 1615  
  
QY 73 cgcgcgcctggctgcaccc-----cgcgcacggttacgcgtgagaagaataat 126  
Db 1614 AGAAGACCATATTGGCACACACCGCGCTTCAGAAACGTTACAGATGCGCGGAAGACG 1555  
  
QY 127 ggcatttcaacacccgcctctccgcaccttcggatatactgtcaagcgcaacacagtc 186  
Db 1554 GGTATCTTCAANTCCCGCCTTTCTACAGAAATTTGTACTACCATATAAAGGA---GGATAC 1498  
  
QY 187 agaacgcctcctggcggtggacatgatgagattcaatataatgactttctccccc 246  
Db 1497 TCGCAGGCATCTTGGATGTTAACTACTCTCAAAATTCACATCGCCGATTCCTCCGCC 1438  
  
QY 247 ggggggggtcaaacccccctctgtgcccccttgaaactactacagaaataagaaggttaag 306  
Db 1437 TCAGGGGACCAACCGCCCTACCCCTACCTTTCATTAATCTACCGTATTAGAAAGGCTAAA 1378  
  
QY 307 gtgaattctggcctgctcccgatcaccagggtgacagggggagtggtccagtgct 366  
Db 1377 TATGAATTTTACCCCGAGAGACCCCATCACCTCTAATCAAGAGGTTGTGGGTCCACGT 1318  
  
QY 367 gttatttagatgaactttgtaacaaaggccacagccctcacctatgacccctatgta 426  
Db 1317 GTTATCTTGATGCCAATTTGTAACCCCTCCACCAACTTGGCTATGACCCCTATATT 1258  
  
QY 427 aactatctcccgccatataccataaccacagccctctctaccaccccggtactttacc 486  
Db 1257 AACTACTCTCCCGCCACACCATAAAGCAGCCCTTTACCTACCACCTCCAGTACTTCACC 1198  
  
QY 487 ccaaacctgtctagatttcactattgattacttccacaaacaaacaaagaaacag 546  
Db 1197 CCCAAACCTGAGCTGGAGACCAAAATTTGATGTGTCCACCCAAATAATAAAGAAACCCAG 1138  
  
QY 547 ctgtgctgagactacaactgctggaaatgtagaccacgtaggcctcgccactgcgttc 606  
Db 1137 CTGTGCTCCTATTAAATACCCACACCAANTGTGAGACACAGCGCCCTCGGTATGCGCTC 1078  
  
QY 607 gaaaacagtatatacagaccggaatacaatatccgtgtaaccatgtatgtacaattcaga 666  
Db 1077 CAAATGTCAGCCACAGCCCAAAATTTATGTGTGAAGGCTGACTATTATTGTACAAATTCAGA 1018  
  
QY 667 gaatttaatttaagaccccccaacttaa 695  
Db 1017 GAATTTATCTTAAAGAGCCCTCTAAATAA 989

RESULT 11  
US-09-347-594-5/c  
; Sequence 5, Application US/09347594  
; Patent No. 6217883  
; GENERAL INFORMATION:  
; APPLICANT: ALLAN, Gordon M.  
; APPLICANT: MEEHAN, Brian M.  
; APPLICANT: ELLIS, John A.  
; APPLICANT: KRAKOWKA, George S.  
; APPLICANT: AUDONNET, Jean-Christophe F.

; TITLE OF INVENTION: PORCINE CIRCOVIRUS AND PARVOVIRUS VACCINE  
; FILE REFERENCE: 454313-2338  
; CURRENT APPLICATION NUMBER: US/09/347,594  
; EARLIER FILING DATE: 1999-07-01  
; EARLIER APPLICATION NUMBER: 98 08777  
; EARLIER FILING DATE: 1998-07-06  
; NUMBER OF SEQ ID NOS: 5  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 5  
; LENGTH: 1759  
; TYPE: DNA  
; ORGANISM: porcine circovirus  
US-09-347-594-5

Query Match 28.4%; Score 199.4; DB 4; Length 1759;  
Best Local Similarity 70.6%; Pred. No. 2.6e-52;  
Matches 266; Conservative 0; Mismatches 111; Indels 0; Gaps 0;  
  
QY 319 cctgtctcccgatcacccagggtgacagggggagtgggctccagtgctgtatttagat 378  
Db 1755 CCCAGAGACCCCATCACCTCTAATCAAGAGGTTGTGGTCCACACTGTTGTTATCTTGGAT 1696  
  
QY 379 gataactttgaacaaaggccacagccctcacctatgacccctatgtaaaactactctcc 438  
Db 1695 GCCAACTTTGTAACCCCTCCACCAACTTGGCTATGACCCCTATATTAACTACTCTCTCC 1636  
  
QY 439 cgcataccataaacccagccctctctaccactcccggtactttacccccaaacctgct 498  
Db 1635 CGCCACACCAATAGCAGCCCTTTACCTACCACTCAGGTACTTCACCCCAACCTGAG 1576  
  
QY 499 ctgatttctactattgatttctccaaacaaacaaacaaacaaacagctgtggtgcaga 558  
Db 1575 CTGGACCAAAACAATGATTGGTTCCACCAATAATAAAGAAACACAGCTGTGGTCCAT 1516  
  
QY 559 ctacaaactgtcgaatgtagaccacgtaggcctcgccactgcgctgcgaaacagata 618  
Db 1515 TTAATATCCCAACCAATGTCGAGCACACAGCCCTCGGCTATGCGCTCCAAAATGCAGCC 1456  
  
QY 619 tacgaccaggaatacaatatccgtgtaaccatgtatgtacaattcagagaatttaatt 678  
Db 1455 ACAGCCCAAAATTTGTTAGGCTGACTATTATGTACAAATTCAGAGAAATTTATCCTA 1396  
  
QY 679 aaagaccccccaacttaa 695  
Db 1395 AAAGACCTCTAAATAA 1379

RESULT 12  
US-09-267-177-22/c  
; Sequence 22, Application US/09267177  
; Patent No. 6287856  
; GENERAL INFORMATION:  
; APPLICANT: Poet, Steven E.  
; APPLICANT: Ritchie, Branson W.  
; APPLICANT: Niagro, Frank D.  
; APPLICANT: Lukert, Phil D.  
; TITLE OF INVENTION: Vaccines against Circovirus Infections  
; FILE REFERENCE: 21099.0057  
; CURRENT APPLICATION NUMBER: US/09/267,177  
; CURRENT FILING DATE: 1999-03-12  
; EARLIER APPLICATION NUMBER: 60/077,890  
; EARLIER FILING DATE: 1998-03-13  
; NUMBER OF SEQ ID NOS: 41  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 22  
; LENGTH: 285  
; TYPE: DNA  
; ORGANISM: porcine circovirus  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)...(285)  
US-09-267-177-22

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Best Local Similarity 67.0%; Pred. No. 4,5e+86;
Matches 470; Conservative 0; Mismatches 222; Indels 9; Gaps 2;

QY 1 atgacgtatccaaggagggtaccgaagaagacacccgccccgcagccatcttggc 60
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 37 atgacgtgccaaggagggtaccgaagaagagaccgccccgcagccatcttggg 96
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 61 cagatctccgcgcgcgcctcgtctgcaccc-----cgcacccttaaccgtgg 114
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 97 aacatctccggaagaccatttggcacaccgccttcagaaacggtacagatgg 156
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 115 agaagaaatggcatcttcaacacccgctctccgcaccttcgatatatactgtcaag 174
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 157 cgcgaagacgggtatcttcaattccgccttctacagaattgtactcacataaaa 216
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 175 cgaacacagtcagaacgcctcgtggcggtggacatgatgagatcaatattaatgac 234
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 217 gga---ggatctcgagccatttggatgttaactacacccaattcaacatcgccag 273
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 235 ttcttccccaggagggggtcaaacccccgcctctgtgccccttggatatactacagaata 294
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 274 ttctccccctcaggcgccacccccctaccctacccttccaatactaccgtatt 333
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 295 agaaggttaagggtgaattctggcctcctcccgatcacccagggtgacaggggagtg 354
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 334 agaaggttaaatatgaattttaccacagagaccccatcacctcttaatacaagaggtgt 393
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 355 ggctccagtgctgtattttagatgataactttgttaacaaaggccacagccctcacctat 414
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 394 gggtccactgtgtattctgttgatgccaaacttgttaacccccctcccaacttggccctat 453
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 415 gacctatgtaaactactctccgcctacacataccacagcccttctctaccactcc 474
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 454 gacctatattaaactactctccgcctacacataaggcagcccttaccaccactcc 513
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 475 cggtaactttacccccaaacctgcttagatttcaacttattgattacttccaaacaaacac 534
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 514 aggtacttcccccaaacctgagtggaacaaacttgaattgttgggtccaccccaataat 573
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 535 aaaaagaaacagctggtgtgagactacaaactgctggaatgtagaccagtaggcctc 594
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 574 aaaaagaaacagctggtgttccatttaataaccacacccaattgctgagcacagggcctc 633
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 595 ggcactgcgttcgaaacagtatatacgcagcaggaatacaatatccgtgtaacctgtat 654
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 634 ggcatacgtccaaaatgcagccacagcccaaaattatgtgtaagcgtgactattat 693
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 655 gtacaattcagagaatttaatttaagacccccccacttaa 695
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 694 gtacaattcagagaatttatctctaaagaccctctaataa 734
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 9
US-09-267-177-25
; Sequence 25, Application US/09267177
; Patent No. 6287856
; GENERAL INFORMATION:
; APPLICANT: Poet, Steven E.
; APPLICANT: Ritchie, Branson W.
; APPLICANT: Niagro, Frank D.
; APPLICANT: Lukert, Phil D.
; TITLE OF INVENTION: Vaccines against Circovirus Infections
; CURRENT APPLICATION NUMBER: US/09/267,177
; CURRENT FILING DATE: 1999-03-12
; EARLIER APPLICATION NUMBER: 60/077,890
; EARLIER FILING DATE: 1998-03-13
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 25
; LENGTH: 897
; TYPE: DNA
; ORGANISM: porcine circovirus
```

```
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(687)
US-09-267-177-25

Query Match 43.2%; Score 303.2; DB 4; Length 687;
Best Local Similarity 67.1%; Pred. No. 7,3e+85;
Matches 463; Conservative 0; Mismatches 218; Indels 9; Gaps 2;

QY 1 atgacgtatccaaggagggttaccgaagaagacacccgccccgcagccatcttggc 60
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1 atgacgtgccaaggagggttaccgaagaagagaccgccccgcagccatcttggg 60
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 61 cagatctccgcgcgcgcctcgtctgcaccc-----cgcacccttaaccgtgg 114
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 61 aacatctccggaagacacatttggcacaccccgcttcagaaacggtacagatgg 120
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 115 agaagaaatggcatcttcaacacccgctctccgcaccttcggatatatactgtcaag 174
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 121 cgcgaagacgggtatcttcaattccgccttctacagaattgtactcacataaaa 180
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 175 cgaacacagtcagaacgcctcctcgtggcggtggacatgatgagatcaatattaatgac 234
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 181 gga---ggatctcgagccatttggatgttaactacacccaattcaacatcgccag 237
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 235 ttcttccccaggagggggtcaaacccccgcctctgtgccccttggatatactacagaata 294
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 238 ttctccccctcaggcgccacccccctaccctacccttccaatactaccgtatt 297
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 295 agaaggttaagggtgaattctggcctcgtcccgatcacccagggtgacaggggagtg 354
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 298 agaaggttaaatatgaattttaccacagagaccccatcacctctaatcaagaggtgtt 357
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 355 ggctccagtgctgtattttagatgataactttgttaacaaaggccacagccctcacctat 414
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 358 gggtccactgtgtattctgttgatgccaaacttgttaacccccctcccaacttggccctat 417
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 415 gacctatgtaaactactctccgcctacacataccacagcccttctctaccactcc 474
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 418 gacctatattaaactactctccgcctacacataaggcagcccttaccaccactcc 477
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 475 cggtaacttaccacccaaacttctctagatttctactattgattcttccaacacaaacac 534
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 478 aggtacttaccacccaaacctgagtggaacaaacaaattgattgttccacccaaataat 537
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 535 aaaaagaaacagctggtggtgagactacaaactcgtggaatgtagaccagtaggcctc 594
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 538 aaaaagaaacagctggtggtccatttaataaccacacccaattgctgagcacacagggcctc 597
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 595 ggcactgcgttcgaaacagtatatacgcagcaggaatacaatatccgtgtaacctgtat 654
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 598 ggctatgcgtcccaaaatgcgcagcagcccaaaattatgtggaagcgtgactattat 657
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 655 gtacaattcagagaatttaatttaaaagac 684
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 658 gtacaattcagagaatttatctctaaagac 687
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 10
US-09-267-177-1/c
; Sequence 1, Application US/09267177
; Patent No. 6287856
; GENERAL INFORMATION:
; APPLICANT: Poet, Steven E.
; APPLICANT: Ritchie, Branson W.
; APPLICANT: Niagro, Frank D.
; APPLICANT: Lukert, Phil D.
; TITLE OF INVENTION: Vaccines against Circovirus Infections
; FILE REFERENCE: 21099.0057
; CURRENT APPLICATION NUMBER: US/09/267,177
; CURRENT FILING DATE: 1999-03-12
; EARLIER APPLICATION NUMBER: 60/077,890
; EARLIER FILING DATE: 1998-03-12
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 25
; LENGTH: 897
; TYPE: DNA
; ORGANISM: porcine circovirus
```

[illegible]

```

Query Match      24.5%; Score 172.2; DB 4; Length 285;
Best Local Similarity 75.8%; Pred. No. 2.8e-44;
Matches 213; Conservative 0; Mismatches 68; Indels 0; Gaps 0;

QY   274 ccctttgaataactacagaataaaaggttaagggtgaaattcggccctgcctccccgatc 333
    ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db    285 CClTTCCAATACACCCTATTGAAAGGCCTAATAATGAATTTTACCCACAGAGACCCCATC 226

QY   334 acccaggggtcacaggggagtgggctcccagtcgttatttagatgataaactttgtaaaca 393
    ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db    225 ACCTCTTAATCAAGAAGGTGTGGTCACACTGTTGTTATCTTGATGCCAACCTTTGTAACC 166

QY   394 agggccacagccctcacctatgaccoccatgtaaaactactcctcccgccatatcataaac 453
    |||| | ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db    165 CCCTCCACCAAACCTTGGCCTATGACCCCTATATTAACTACTCTCTCCGCCCACCATAAAG 106

QY   454 cagccctctctcaacctcccgggtactttaacccccaaaaacctgcctcctagtatttcatt 513
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db    105 CAGCGCCTTTACCTACCACCTCCAGGTACTTCACCCCCAACCTGAGCTGGACCAACAATT 46

QY   514 gattacttccaaccaaacaaagaagaacacagctgtggct 554
    |||| | ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db     45 GATTGGTTCCACCNAATATAAAGAAACACAGCTGTGGCT 5

RESULT 13
US-09-103-840A-2/c
; Sequence 2, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; TITLE OF INVENTION: TUBERCULOSIS
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 2
; LENGTH: 4403765
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; FEATURE:
; OTHER INFORMATION: CDC 1551
; OTHER INFORMATION: "n" bases at various positions throughout the sequence
; OTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2

Query Match      6.4%; Score 44.6; DB 4; Length 4403765;
Best Local Similarity 56.5%; Pred. No. 0.033;
Matches 83; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

QY   10 ccaagaggggttacgagaagaagaacacgccccccgacgcatcttgtgccagatcctc 69
    ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db    2690630 CCCCGCCGCGCGCGCGATGTCGGAAGAGACCCGCGCGCGCGCGCCGACCCGC 2690571

QY   70 cgpcgcgcgcctggctcgtccacccccgcacgcttacgcctggagagaaaaatgac 129
    ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db    2690570 CGCGGCCGCTCCGGGTAAGTCGTGGCGCGCGCGCGGTGCCGCGGTGCCGATCAAGATGC 2690511

QY   130 attctcaaacaccgcctctctccgcacc 156
    ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db    2690510 GC CGCGGCCCGCGCGCGCGCTCC 2690484

RESULT 14
US-09-117-121-41

```



GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 23, 2002, 07:34:24 ; Search time 1780.41 Seconds  
(without alignments)  
5321.731 Million cell updates/sec

Title: US-09-514-245B-25

Perfect score: 702

Sequence: 1 atgacgtatccaaggagcg.....acccccacttaaccccttaa 702

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:\*

1: em\_estba:\*  
2: em\_esthum:\*  
3: em\_estin:\*  
4: em\_estmu:\*  
5: em\_estov:\*  
6: em\_estpl:\*  
7: em\_estro:\*  
8: em\_htc:\*  
9: gb\_est1:\*  
10: gb\_est2:\*  
11: gb\_htc:\*  
12: gb\_gss:\*  
13: em\_gss\_hum:\*  
14: em\_gss\_inv:\*  
15: em\_gss\_pln:\*  
16: em\_gss\_vrt:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	45.4	6.5	561	9 AI514058	AI514058 GH27112.5
C 2	44.6	6.4	939	12 CNS01608	AL059400 Drosophila
C 3	44.2	6.3	638	10 BI629442	BI629442 RH58310.5
C 4	44.4	6.3	445	9 AI292664	AI292664 GH15617.5
C 5	44.4	6.3	484	9 AI108264	AI108264 GH07058.5
C 6	44.4	6.3	493	9 AI405757	AI405757 GH25879.5
C 7	44.4	6.3	497	9 AI238309	AI238309 GH14332.5
C 8	44.4	6.3	532	9 AI134557	AI134557 GH12051.5
C 9	44.4	6.3	557	9 AI404106	AI404106 GH23705.5
C 10	44.4	6.3	557	9 AI406114	AI406114 GH26313.5
C 11	44.4	6.3	558	9 AI238565	AI238565 GH14632.5
C 12	44.4	6.3	561	9 AI404901	AI404901 GH24758.5
C 13	44.4	6.3	561	9 AI406248	AI406248 GH26478.5
C 14	44.4	6.3	575	9 AI403207	AI403207 GH22602.5
C 15	44.4	6.3	593	9 AI516823	AI516823 GH27392.5
C 16	44.4	6.3	597	10 BI627948	BI627948 RH69450.5
C 17	44.4	6.3	613	9 AI237965	AI237965 GH13172.5

C 18	43.8	6.2	554	9 AI293059	AI293059 GH16139.5
C 19	43.4	6.2	870	10 BG445569	BG445569 GA_Ea002
C 20	43.4	6.2	479	9 AI402428	AI402428 GH21648.5
C 21	43.2	6.2	521	9 AA530753	AA530753 vJ44e07.1
C 22	43.2	6.2	555	9 AI296628	AI296628 LP10591.5
C 23	43.2	6.2	574	10 BI619435	BI619435 RH50489.5
C 24	43.2	6.2	575	10 BI619848	BI619848 RH50971.5
C 25	43.2	6.2	591	9 AI857154	AI857154 603007B08
C 26	43.2	6.2	835	11 AK020691	AK020691 Mus muscu
C 27	43	6.1	452	9 AA589477	AA589477 vL47h12.8
C 28	43	6.1	514	9 AA798859	AA798859 vV94a07.1
C 29	43	6.1	617	10 BG591496	BG591496 EST499338
C 30	43	6.1	636	9 AA698799	AA698799 HL05714.5
C 31	43	6.1	650	10 BG599848	BG599848 EST504743
C 32	43	6.1	706	10 BM110666	BM110666 EST558202
C 33	43	6.1	710	10 BF253141	BF253141 EST445636
C 34	42.8	6.1	1064	12 CNS01608	AI51849 Anopheles
C 35	42.6	6.1	449	9 AW615354	AW615354 hh74b04.x
C 36	42.6	6.1	494	9 AI141028	AI141028 Oy68h12.x
C 37	42.6	6.1	496	9 AI364938	AI364938 qz23d02.x
C 38	42.6	6.1	574	10 BI799844	BI799844 H142B04.E
C 39	42.6	6.1	575	10 C99980	C99980 C99980 Oryz
C 40	42.6	6.1	592	9 AI017603	AI017603 ou29e09.x
C 41	42.6	6.1	657	10 BI561078	BI561078 603254284
C 42	42.4	6.0	459	9 AU181814	AU181814 AU181814
C 43	42.4	6.0	580	9 AI238831	AI238831 GH14954.5
C 44	42.4	6.0	653	10 BI614132	BI614132 RH43436.5
C 45	42.4	6.0	655	10 BI750241	BI750241 F902_06b0

## ALIGNMENTS

RESULT 1  
AI514058/c

LOCUS

DEFINITION

AI514058.1 GI:4418120

ACCSSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

AI514058 561 bp mRNA linear EST 19-APR-2001  
GH27112.5prime GH Drosophila melanogaster head p0T2 Drosophila  
melanogaster cdna clone GH27112 5prime, mRNA sequence.

AI514058

AI514058.1 GI:4418120

fruit fly.

Drosophila melanogaster

Eukaryota: Metazoa: Arthropoda: Tracheata: Hexapoda: Insecta;

Pterygota: Neoptera: Endopterygota; Diptera; Brachycera;

Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 561)

Harvey,D., Brokstein,P., Hong,L., Evans-Holm,M., Su,C., Tsang,G.,

Lewis,S. and Rubin,G.M.

BDGP/HMI Drosophila EST Project

Unpublished (2001)

Contact: Stapleton, M.

BDGP

Lawrence Berkeley National Lab

One Cyclotron Rd. Berkeley, CA 94720, USA

Fax: 510 486 6798

Email: <http://www.fruitfly.org/EST>, [est@fruitfly.berkeley.edu](mailto:est@fruitfly.berkeley.edu)

Plate: 271 row: A column: 12

High quality sequence stop: 488.

Location/Qualifiers

1..561

/organism="Drosophila melanogaster"

/db\_xref="taxon:7227"

/clone="GH27112"

/sex="male and female"

/dev\_stage="adult"

/lab\_host="DHS - alpha"

/note="Organ: head; Vector: p0T2; Site:1: EcoRI; Site:2:

XhoI; Sized fractionated cDNAs were directly ligated into

p0T2. Plasmid cDNA library."

74 a 110 c 244 g 133 t

BASE COUNT

ORIGIN



```

Query Match          6.5%; Score 45.4; DB 9; Length 561;
Best Local Similarity 58.5%; Pred. No. 0.89;
Matches 79; Conservative 0; Mismatches 56; Indels 0; Gaps 0;

QY 32 gaagacacgccccgagccatcttgccagatcctccgcgccgccccctggctgctcc 91
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 560 GCAGATTCCACCGCTCCACGAGATGGCCACCTCCGCCGCCGATTCGCCACCAATCC 501
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 92 accccgcccacgcttaccgctggaggaagaaaatggcatcttcaaacaccgcctctccc 151
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 500 AGGGCGCCACCGATTCCGCTACCTCCACCAGATGGCCACCTCCACCGCGGATCCGCC 441
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 152 gcaccttcggatata 166
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 440 ACCTCCTCCGGAATA 426
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 2
CNS000CNG          939 bp DNA linear GSS 04-JUN-1999
LOCUS              Drosophila melanogaster genome survey sequence TET3 end of BAC #
DEFINITION         BACR26H16 of RPCI-98 library from Drosophila melanogaster (fruit
fly); genomic survey sequence.
ACCESSION          AL059400
VERSION            AL059400.1 GI:4946964
KEYWORDS            GSS.
SOURCE             fruit fly.
ORGANISM            Drosophila melanogaster
                   Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
                   Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
                   Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE           1 (bases 1 to 939)
AUTHORS             Genoscope.
TITLE              Direct Submission
JOURNAL            Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
                   BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
                   - Web : www.genoscope.cns.fr)
COMMENT             Determination of this BAC-end sequence was carried out as part of a
                   collaboration with the Berkeley Drosophila Genome Project (BDGP).
                   The BDGP is constructing a physical map of the Drosophila
                   melanogaster genome using these BACs. For further information
                   please see http://www.fruitfly.org The BDGP Drosophila
                   melanogaster BAC library was prepared by Kazutoyo Osoegawa and
                   Aaron Mammoser in Pieter de Jong's laboratory in the Department of
                   Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
                   NY. The library is named RPCI-98 and was constructed by partial
                   EcoRI digestion of Drosophila DNA provided by the BDGP from the
                   isogenic strain Y2; cn bw sp, the same strain used for the BDGP's
                   p1 and EST libraries. A more detailed description of the library
                   and how to order individual BAC clones, the entire library, or
                   filters for hybridization from the BACPAC Resource Center can be
                   found at http://bacpac.med.buffalo.edu/drosophila\_bac.htm.
FEATURES             Location/Qualifiers
                   1..939
                   /organism="Drosophila melanogaster"
                   /db_xref="taxon:7227"
                   /clone_lib="RPCI-98"
                   /clone="BACR26H16"
                   /note="end : TET3"
BASE COUNT          71 a 349 c 104 g 180 t 235 others
ORIGIN

Query Match          6.4%; Score 44.6; DB 12; Length 939;
Best Local Similarity 18.1%; Pred. No. 1.6;
Matches 56; Conservative 122; Mismatches 131; Indels 0; Gaps 0;

QY 391 aaaaaggccacagccctcacctatgacccctatgtaaactactctctccgcataccata 450
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 274 MMHAMWMCCTTCCTCCGCMCTCCGCCCCCAATCCGCMCCCTCTTCCTCCATCCMMC 333
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

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QY 451 accagcccttctctaccactccggtactttaccaccaaacctgtctctagatttcaact 510
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 334 CCTCTCCCCCCTATCCCTCTCMMYHTTMMCCCTCCCTCCMMCHMTCCMMMMMM 393
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 511 atgtattacttccaacaaacaaagaacacagctgtggtctgagactacaactgct 570
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 394 MMMMMMTTMMMMMMMMMTMMHMMMTTMMHMMMTTMMHMMMTTMMHMMMTTMMHMM 453
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 571 ggaatgttagaccagctgagcctgcgcactgcgttcgaacacagtatatacacaccagga 630
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 454 MMMMMMMMTTMMMMMMMTTMMHMMMTTMMHMMMTTMMHMMMTTMMHMMMTTMMHMM 513
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 631 tacaatacctgtagaacatgtatgtacaattcacagaagaatttaatttaaacagcccca 690
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 514 MMMMMMTTMMMTTMMMMMMMTTMMHMMMTTMMHMMMTTMMHMMMTTMMHMMMTTMMT 573
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 691 cttaaacct 699
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 574 CGTCTCTCT 582
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 3
BI629442          638 bp mRNA linear EST 10-SEP-2001
LOCUS              RH58310.5prime RH Drosophila melanogaster normalized Head pFlc-1
DEFINITION         Drosophila melanogaster cDNA clone RH58310 5 similar to CG17108:
                   FBan0017108 GO:[ ] located on: 2L 32A1-32A1:: 08/23/2001, mRNA
                   sequence.
ACCESSION          BI629442
VERSION            BI629442.1 GI:15531652
KEYWORDS            EST.
SOURCE             fruit fly.
ORGANISM            Drosophila melanogaster
                   Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
                   Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
                   Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE           1 (bases 1 to 638)
AUTHORS             Stapleton,M., Brokstein,P., Hong,L., Tyler,D., Berman,B., Carlson
                   ,J., Champe,M., Chavez,C., Dorsett,V., Farfan,D., Frise,E., George
                   ,R., Gonzalez,M., Guarin,H., Harris,N., Li,P., Liao,G., Mista,S.,
                   Mungall,C.J., Nunoo,J., Pacleb,J., Paragas,V., Park,S.,
                   Phouanavong,S., Wan,K., Yu,C., Lewis,S.E., Celniker,S. and Rubin
                   ,G.M.
TITLE              BDGP/HHMI RH Drosophila EST Project
JOURNAL            Unpublished (2001)
COMMENT             Contact: Stapleton, M.
                   BDGP
                   Lawrence Berkeley National Lab
                   One Cyclotron Rd, Berkeley, CA 94720, USA
                   Fax: 510 486 6798
                   Email: http://www.fruitfly.org/EST\_est@fruitfly.berkeley.edu
                   hit genomic AE003629: arm:2L [10413221,10674011]
                   estimated-cyto:3LE5-32A5: 08/23/2001
                   Plate: RH.583 row: A column: 10
                   High quality sequence stop: 511.
FEATURES             Location/Qualifiers
                   1..638
                   /organism="Drosophila melanogaster"
                   /db_xref="taxon:7227"
                   /clone="RH58310"
                   /clone_lib="RH Drosophila melanogaster normalized Head
                   pFlc-1"
                   /sex="male and female"
                   /dev_stage="Adult"
                   /lab_host="DH5-alpha TonA"
                   /note="Organ: head; Vector: pFlc1; Site:1: XhoI; Site:2:
                   BamHI; Library was kindly generated by Piero Carninci at
                   the RIKEN. The library was normalized and excised using
                   Cre recombinase. Plasmid cDNA library."
BASE COUNT          87 a 127 c 269 g 153 t 2 others
ORIGIN

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FEATURES	High quality sequence stop: 457.
source	Location/Qualifiers
	1. .497
	/organism="Drosophila melanogaster"
	/db_xref="taxon:7227"
	/clone="GH14332"
	/clone_lib="GH Drosophila melanogaster head pot2"
	/sex="male and female"
	/dev_stage="adult"
	/lab_host="DH5 - alpha"
	/note="Organ: head; Vector: pot2; Site_1: EcoRI; Site_2: XhoI; Sized fractionated cDNAs were directly ligated into pot2. Plasmid cDNA library."
BASE COUNT	80 a 96 c 222 g 99 t
ORIGIN	

[illegible]

Db		61	TCTCCGGAATA	50	
RESULT	8				
LOCUS	A1134557/c				
DEFINITION	A1134557 532 bp mRNA linear EST 19-APR-2001 GH12051.5prime GH Drosophila melanogaster head pot2 Drosophila melanogaster cDNA clone GH12051 5prime, mRNA sequence.				
ACCESSION	A1134557				
VERSION	A1134557.1				
KEYWORDS	EST.				
SOURCE	fruit fly.				
ORGANISM	Drosophila melanogaster				
	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterivota; Neoptera; Endopterygota; Diptera; Brachycera;				

```

I (bases 1 to 352)
Harvey,D., Brokstein,P., Hong,L., Evans-Holm,M., Su,C., Tsang,G.,
Lewis,S. and Rubin,G.M.
BDGP/HHMI Drosophila EST Project
Unpublished (2001)
Contact: Stapleton, M.
BDGP
Lawrence Berkeley National Lab
One Cyclotron Rd, Berkeley, CA 94720, USA
Fax: 510 486 6798
Email: http://www.fruitfly.org/EST\_est@fruitfly.berkeley.edu
Plate: 120 row: E column: 3
High quality sequence stop: 403.
Location/Qualifiers
1. 532
/organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/clones="GH12031"
/clone_lib="GH Drosophila melanogaster head pot2"
/sex="male and female"
/dev_stage="adult"
/lab_host="DH5 - alpha"
/notice="Organ: head; Vector: pot2; Site: EcORT; Site:2:
xhoI; Sized fractionated cDNAs were directly ligated into
pot2. Plasmid cDNA library."
93 a 101 c 234 q 124 t
73 a 101 c 234 q 124 t

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Query Match      6.3%; Score 44.2; DB 10; Length 638;
Best Local Similarity 57.2%; Pred. No. 1.8;
Matches 79; Conservative 0; Mismatches 59; Indels 0; Gaps 0;

QY 29 gaagaagacaccccccagccatcttgccagatctcccgccgcccctggctcg 88
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 581 GCGCCGATTCCACCGCTCCACAGATGGCCACCTCCCGCCGGATTCCGCCACCAA 522
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 89 tcacaccccccagcccttaccgctggagaagaaaatggcatcttcaacacccgcctct 148
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 521 TCAGGGCGCCACCGATTCCGCTACTCTCCACAGATGCCACCTCCACCGCGATTCC 462

QY 149 ccgcgaccttcggatata 166
    | | | | | | | | | |
Db 461 GCACCTCTCTCCGGAATA 444

RESULT 4
AI292664/c
LOCUS
DEFINITION
  GH15617.5prime GH Drosophila melanogaster head pOT2 Drosophila
  melanogaster cdna clone GH15617 5prime, mRNA sequence.
ACCESSION
  AI292664
VERSION
  AI292664.1 GI:3942071
KEYWORDS
  EST.
SOURCE
  fruit fly.
ORGANISM
  Drosophila melanogaster
  Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
  Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
  Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE
  1 (bases 1 to 445)
  Harvey,D., Brokstein,P., Hong,L., Evans-Holm,M., Su,C., Tsang,G.,
  Lewis,S. and Rubin,G.M.
  BDCP/HMI Drosophila EST Project
  Unpublished (2001)
  Contact: Stapleton, M.
  BDCP
  Lawrence Berkeley National Lab
  One Cyclotron Rd, Berkeley, CA 94720, USA
  Fax: 510 486 6798
  Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
  Plate: 156 row: B column: 5
  High quality sequence stop: 293.
FEATURES
  source
  1..445
  /organism="Drosophila melanogaster"
  /db_xref="taxon:7227"
  /clone="GH15617"
  /sex="male and female"
  /dev_stage="adult"
  /lab_host="DH5 - alpha"
  /note="Organ: head; Vector: pOT2; Site:1: EcoRI; Site_2:
  XhoI; Sized fractionated cDNAs were directly ligated into
  pOT2. Plasmid cdna library."
  pOT2. Plasmid cdna library."
  64 a 87 c 193 g 101 t

Query Match      6.3%; Score 44; DB 9; Length 445;
Best Local Similarity 58.3%; Pred. No. 1.9;
Matches 77; Conservative 0; Mismatches 55; Indels 0; Gaps 0;

QY 35 gacacgccccgagccatcttgccagatctccgcccgcgcctggctcgctccacc 94
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 389 GATTCCCGCTCCACAGATGGCCACCTCCCGCCGGATTCCGCCACCAATCCAGG 330
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 95 ccgcgacccgttaccgctggagaagaaaatggcatcttcaacacccgcctctccgca 154
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 329 GCGGCCACCGATTCCGCTACTCTCCACAGATGGCCACCTCCACCGCGATTCCGCCACC 270
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 155 ccttcggatata 166
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Db 269 TCCTCCGGAATA 258

RESULT 5
AI108264/c
LOCUS
DEFINITION
  GH07058.5prime GH Drosophila melanogaster head pOT2 Drosophila
  melanogaster cdna clone GH07058 5prime, mRNA sequence.
ACCESSION
  AI108264
VERSION
  AI108264.1 GI:3476543
KEYWORDS
  EST.
SOURCE
  fruit fly.
ORGANISM
  Drosophila melanogaster
  Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
  Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
  Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE
  1 (bases 1 to 484)
  Harvey,D., Brokstein,P., Hong,L., Evans-Holm,M., Su,C., Tsang,G.,
  Lewis,S. and Rubin,G.M.
  BDCP/HMI Drosophila EST Project
  Unpublished (2001)
  Contact: Stapleton, M.
  BDCP
  Lawrence Berkeley National Lab
  One Cyclotron Rd, Berkeley, CA 94720, USA
  Fax: 510 486 6798
  Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
  Plate: 70 row: E column: 10
  High quality sequence stop: 404.
FEATURES
  source
  1..484
  /organism="Drosophila melanogaster"
  /db_xref="taxon:7227"
  /clone="GH07058"
  /sex="male and female"
  /dev_stage="adult"
  /lab_host="DH5 - alpha"
  /note="Organ: head; Vector: pOT2; Site:1: EcoRI; Site_2:
  XhoI; Sized fractionated cDNAs were directly ligated into
  pOT2. Plasmid cdna library."
  pOT2. Plasmid cdna library."
  69 a 88 c 212 g 115 t

Query Match      6.3%; Score 44; DB 9; Length 484;
Best Local Similarity 58.3%; Pred. No. 1.9;
Matches 77; Conservative 0; Mismatches 55; Indels 0; Gaps 0;

QY 35 gacacgccccgagccatcttgccagatctccgcccgcgcctggctcgctccacc 94
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 401 GATTCCCGCTCCACAGATGGCCACCTCCCGCCGGATTCCGCCACCAATCCAGG 342
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 95 ccgcgacccgttaccgctggagaagaaaatggcatcttcaacacccgcctctccgca 154
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 341 GCGGCCACCGATTCCGCTACTCTCCACAGATGGCCACCTCCACCGCGATTCCGCCACC 282
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 155 ccttcggatata 166
    | | | | | | | | | |
Db 281 TCCTCCGGAATA 270

RESULT 6
AI405757/c
LOCUS
DEFINITION
  GH25879.5prime GH Drosophila melanogaster head pOT2 Drosophila
  melanogaster cdna clone GH25879 5prime, mRNA sequence.
ACCESSION
  AI405757
VERSION
  AI405757.1 GI:4248844
KEYWORDS
  EST.
SOURCE
  fruit fly.
ORGANISM
  Drosophila melanogaster
  Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

```

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SOURCE
ORGANISM
fruit fly.
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE
1 (bases 1 to 558)
AUTHORS
Harvey,D., Brokstein,P., Hong,L., Evans-Holm,M., Su,C., Tsang,G.,
Lewis,S. and Rubin,G.M.
TITLE
BDGP/HHMI Drosophila EST Project
JOURNAL
Unpublished (2001)
COMMENT
Contact: Stapleton, M.
BDGP
Lawrence Berkeley National Lab
One Cyclotron Rd, Berkeley, CA 94720, USA
Fax: 510 486 6798
Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
Plate: 146 row: C column: 8
High quality sequence stop: 489.
Location/Qualifiers
1..558
/organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/clone_lib="GH14632"
/clone_lib="GH Drosophila melanogaster head pot2"
/sex="male and female"
/dev_stage="adult"
/lab_host="DH5 - alpha"
/note="Organ: head; Vector: pOT2; Site:1: EcoRI; Site_2:
XhoI; Sized fractionated cDNAs were directly ligated into
pOT2. Plasmid cDNA library."
BASE COUNT      75 a  109 c  241 g  133 t
ORIGIN
Query Match      6.3%; Score 44; DB 9; Length 558;
Best Local Similarity 58.3%; Pred. No. 2;
Matches 77; Conservative 0; Mismatches 55; Indels 0; Gaps 0;

Qy 35 gacacgccccgcagccatcttgccagatcctccgcgcgcgcctggctgcacc 94
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Db 558 GATTCCACCGCTCCACCAAGATGCCACATCCCGCGCGATTCCGCCACCAATCCAGG 499

Qy 95 ccgcgcccttaccgctggagaggaaaatggcatcttcaacacccgcctctcccgca 154
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 498 GCGGCCACCGATTCCGCTACTCTCCACCAAGATGCCACCTCCACCGCGATTCCGCCACC 439

Qy 155 ccttcggatata 166
    ||| ||| |||
Db 438 TCCTCCGGGAATA 427

RESULT 12
AI404901/C
LOCUS
DEFINITION
AI404901.1 561 bp mRNA linear EST 19-APR-2001
melanogaster cDNA clone GH24758 5prime, mRNA sequence.
ACCESSION
AI404901
VERSION
AI404901.1 GI:4247988
KEYWORDS
EST.
SOURCE
fruit fly.
ORGANISM
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE
1 (bases 1 to 561)
AUTHORS
Harvey,D., Brokstein,P., Hong,L., Evans-Holm,M., Su,C., Tsang,G.,
Lewis,S. and Rubin,G.M.
TITLE
BDGP/HHMI Drosophila EST Project
JOURNAL
Unpublished (2001)
COMMENT
Contact: Stapleton, M.
BDGP
Lawrence Berkeley National Lab
One Cyclotron Rd, Berkeley, CA 94720, USA
Fax: 510 486 6798
Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
Plate: 264 row: G column: 6
High quality sequence stop: 494.
Location/Qualifiers
1..561
/organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/clone_lib="GH24758"
/clone_lib="GH Drosophila melanogaster head pot2"
/sex="male and female"
/dev_stage="adult"
/lab_host="DH5 - alpha"
/note="Organ: head; Vector: pOT2; Site_1: EcoRI; Site_2:
XhoI; Sized fractionated cDNAs were directly ligated into
pOT2. Plasmid cDNA library."
BASE COUNT      74 a  110 c  245 g  132 t
ORIGIN
Query Match      6.3%; Score 44; DB 9; Length 561;
Best Local Similarity 58.3%; Pred. No. 2;
Matches 77; Conservative 0; Mismatches 55; Indels 0; Gaps 0;

Qy 35 gacacgccccgcagccatcttgccagatcctccgcgcgcgcctggctgcacc 94
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 558 GATTCCACCGCTCCACCAAGATGCCACCTCCCGCGCGATTCCGCCACCAATCCAGG 499

Qy 95 ccgcgcccttaccgctggagaggaaaatggcatcttcaacacccgcctctcccgca 154
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 498 GCGGCCACCGATTCCGCTACTCTCCACCAAGATGCCACCTCCACCGCGATTCCGCCACC 439

Qy 155 ccttcggatata 166
    ||| ||| |||
Db 438 TCCTCCGGGAATA 427

RESULT 13
AI406248/C
LOCUS
DEFINITION
AI406248 561 bp mRNA linear EST 19-APR-2001
melanogaster cDNA clone GH26478 5prime, mRNA sequence.
ACCESSION
AI406248
VERSION
AI406248.1 GI:4249335
KEYWORDS
EST.
SOURCE
fruit fly.
ORGANISM
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE
1 (bases 1 to 561)
AUTHORS
Harvey,D., Brokstein,P., Hong,L., Evans-Holm,M., Su,C., Tsang,G.,
Lewis,S. and Rubin,G.M.
TITLE
BDGP/HHMI Drosophila EST Project
JOURNAL
Unpublished (2001)
COMMENT
Contact: Stapleton, M.
BDGP
Lawrence Berkeley National Lab
One Cyclotron Rd, Berkeley, CA 94720, USA
Fax: 510 486 6798
Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
Plate: 264 row: G column: 6
High quality sequence stop: 494.
Location/Qualifiers
1..561
/organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/clone_lib="GH26478"
/clone_lib="GH Drosophila melanogaster head pot2"
/sex="male and female"
/dev_stage="adult"
/lab_host="DH5 - alpha"
/note="Organ: head; Vector: pOT2; Site_1: EcoRI; Site_2:
XhoI; Sized fractionated cDNAs were directly ligated into
pOT2. Plasmid cDNA library."
FEATURES
source
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/organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/clone_lib="GH24758"
/clone_lib="GH Drosophila melanogaster head pot2"
/sex="male and female"
/dev_stage="adult"
/lab_host="DH5 - alpha"
/note="Organ: head; Vector: pOT2; Site_1: EcoRI; Site_2:
XhoI; Sized fractionated cDNAs were directly ligated into
pOT2. Plasmid cDNA library."

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GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 23, 2002, 07:43:54 ; Search time 268.88 Seconds  
(without alignments)  
4482.572 Million cell updates/sec

Title: US-09-514-245B-25  
Perfect score: 702  
Sequence: 1 atgacgtatcaaggaggcg.....acccccacttaacccttaa 702

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N\_Geneseq\_032802.\*

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- 2: /SID55/gcgdata/geneseq/geneseq-emb1/NA1981.DAT.\*
- 3: /SID55/gcgdata/geneseq/geneseq-emb1/NA1982.DAT.\*
- 4: /SID55/gcgdata/geneseq/geneseq-emb1/NA1983.DAT.\*
- 5: /SID55/gcgdata/geneseq/geneseq-emb1/NA1984.DAT.\*
- 6: /SID55/gcgdata/geneseq/geneseq-emb1/NA1985.DAT.\*
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- 9: /SID55/gcgdata/geneseq/geneseq-emb1/NA1988.DAT.\*
- 10: /SID55/gcgdata/geneseq/geneseq-emb1/NA1989.DAT.\*
- 11: /SID55/gcgdata/geneseq/geneseq-emb1/NA1990.DAT.\*
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- 14: /SID55/gcgdata/geneseq/geneseq-emb1/NA1993.DAT.\*
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- 20: /SID55/gcgdata/geneseq/geneseq-emb1/NA1999.DAT.\*
- 21: /SID55/gcgdata/geneseq/geneseq-emb1/NA2000.DAT.\*
- 22: /SID55/gcgdata/geneseq/geneseq-emb1/NA2001A.DAT.\*
- 23: /SID55/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT.\*
- 24: /SID55/gcgdata/geneseq/geneseq-emb1/NA2002.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	622	88.6	2520	22	AAF75827 Plasmid pJP102 DNA
2	622	88.6	2520	22	AAF75817 pJP102 donor plasm
3	622	88.6	2769	22	AAF75830 Plasmid pJP107 DNA
4	622	88.6	3609	22	AAF75832 pJP107 donor plasm
5	620.4	88.4	1768	20	AAK83754 Porcine circovirus
6	617.2	87.9	1768	22	AAF75841 PCV DNA fragment o
7	612.4	87.2	1768	22	AAF75840 PCV DNA fragment o
8	595.6	84.8	1786	20	AAK83755 Porcine circovirus
9	590.8	84.2	1361	20	AAK83757 Porcine circovirus

C 10	381.6	54.4	1767	20	AAK35378 Nucleotide sequenc
C 11	381.6	54.4	1767	20	AAK35210 Nucleotide sequenc
C 12	381.6	54.4	1767	21	AAZ56869 DNA sequence of PC
C 13	381.6	54.4	1767	22	AAF75835 PCV DNA fragment o
C 14	378.4	53.9	1767	20	AAK35379 Nucleotide sequenc
C 15	378.4	53.9	1767	20	AAK35211 Nucleotide sequenc
C 16	378.4	53.9	1767	21	AAZ56870 DNA sequence of PC
C 17	378.4	53.9	1767	22	AAF75836 PCV DNA fragment o
C 18	340	48.4	1768	20	AAK35380 Nucleotide sequenc
C 19	340	48.4	1768	20	AAK35381 Nucleotide sequenc
C 20	340	48.4	1768	20	AAK35213 Nucleotide sequenc
C 21	340	48.4	1768	20	AAK35212 Nucleotide sequenc
C 22	340	48.4	1768	21	AAZ56871 DNA sequence of PC
C 23	340	48.4	1768	21	AAZ56872 DNA sequence of PC
C 24	340	48.4	1768	22	AAF75837 PCV DNA fragment o
C 25	340	48.4	1768	22	AAF75838 PCV DNA fragment o
C 26	339	48.3	1768	20	AAK35382 Nucleotide sequenc
C 27	339	48.3	1768	20	AAK35012 Genomic DNA sequen
C 28	339	48.3	1768	20	AAK35214 Nucleotide sequenc
C 29	311	44.3	1759	20	AAK85593 Nucleotide sequenc
C 30	307.8	43.8	1759	20	AAH79992 Porcine circovirus
C 31	273.4	38.9	7460	22	AAH74867 Nucleotide sequenc
C 32	256.4	36.5	5285	22	AAH74865 Nucleotide sequenc
C 33	256.4	36.5	5650	22	AAH74866 Nucleotide sequenc
C 34	203.6	29.0	1759	20	AAK35013 Nucleotide sequen
C 35	199.4	28.4	1759	22	AAF75839 DNA fragment of PK
C 36	44.6	6.4	4403765	22	AAI99683 Mycobacterium tube
C 37	44	6.3	1181	23	ABL24269 Drosophila melanog
C 38	44	6.3	4905	23	ABL24268 Drosophila melanog
C 39	43.4	6.2	10348	22	ABA08714 Human Huntington's
C 40	42.6	6.1	592	21	AAZ93361 Sequence encoding
C 41	41.8	6.0	322	18	AAZ75508 P. americanus anti
C 42	41.8	6.0	322	21	AAZ49961 Winter flounder li
C 43	41.8	6.0	322	20	AAK18930 Human huntingtin g
C 44	41.8	6.0	1371	18	AAZ78974 Mouse Huntington's
C 45	41.8	6.0	9997	18	AAZ97925 Composite sequence

ALIGNMENTS

RESULT 1

AAF75827

ID AAF75827 standard; DNA; 2520 BP.

XX

AC AAF75827;

XX

DT 18-MAY-2001 (first entry)

XX

DE Plasmid pJP102 DNA fragment.

XX

KW ALVAC; porcine circovirus-2; vaccine; pig; myocarditis; abortion;

KW Intrauterine infection; multisystemic wasting syndrome; ds.

XX

OS Unidentified.

XX

PN WO200116330-A2.

XX

PD 08-MAR-2001.

XX

PF 28-AUG-2000; 2000WO-EP08781.

XX

PR 31-AUG-1999; 99US-0151564.

PR 31-MAY-2000; 2000US-0583350.

XX

PA (MERI-) MERIAL.

PA (UYSA-) UNIV SASKATCHEWAN.

PA (UYBE-) UNIV QUEENS BELFAST.

XX

PI Ellis JA, Allan GM, Meehan B, Clark E, Haines D, Hassard L;

PI Harding J, Charreyre CE, Chappuis GE, Krakowka GS, Audonnet JF;

PI Mcneilly F;

XX





QY 301 gttaaagttgaattcttggccctgctcccgatcaccagaggttaacaggagtgagctcc 360  
|||||  
Db 1702 gttaaagttgaattcttggccctgctcccgatcaccagaggttaacaggagtgagctcc 1761  
QY 361 agtgcgttatttttagatgataaactttgtacaagaagccacagccctcacctatgacccc 420  
|||||  
Db 1762 actgcgttatttttagatgataaactttgtacaagaagccacagccctcacctatgacccc 1821  
QY 421 tatgtaaactactctctccgcgcatacacaataccacagccctctctctaccactccggtac 480  
|||||  
Db 1822 tatgtaaactactctctccgcgcatacacaataccacagccctctctctaccactccggtac 1881  
QY 481 tttaaccccaaaactctctagatttactattgattacttccaaacaaacaaaga 540  
|||||  
Db 1882 ttcaaccccaaaactctctagatttactattgattacttccaaacaaacaaaga 1941  
QY 541 aaccagctgtggctgagactacaaaactgtggaattgtagacacgtaggcctcgccact 600  
|||||  
Db 1942 aatcagcttggctgagactacaaaactctggaattgtgacacgtaggcctcgccact 2001  
QY 601 gogtgcgaacacagttatcacgaccaggaatacaatatccgtgttaaccatgtatgtacaa 660  
|||||  
Db 2002 gogtgcgaacacagttatcacgaccaggaatacaatatccgtgttaaccatgtatgtacaa 2061  
QY 661 ttcagagaatttaatttaaagaccccccaacttaacccttaa 702  
Db 2062 ttcagagaatttaatttaaagaccccccaacttaacccttaa 2103

RESULT 3

AAAF75830/c  
ID AAF75830 standard; DNA; 2769 BP.  
XX  
AC  
XX AAF75830;  
XX  
DT 18-MAY-2001 (first entry)  
XX  
DE Plasmid pJP107 DNA fragment.  
XX  
XX ALVAC; porcine circovirus-2; vaccine; pig; myocarditis; abortion;  
KW intrauterine infection; multisystemic wasting syndrome; ds.  
XX  
XX Unidentified.  
XX  
PN WO200116330-A2.  
XX  
PD 08-MAR-2001.  
XX  
PF 28-AUG-2000; 2000WO-EF08781.  
XX  
PR 31-AUG-1999; 99US-0151564.  
PR 31-MAY-2000; 2000US-0583350.  
XX  
PA (MERI-) MERIAL.  
PA (UYSA-) UNIV SASKATCHEWAN.  
PA (UYBE-) UNIV QUEENS BELFAST.  
XX  
PI Ellis JA, Allan GM, Meehan B, Clark E, Haines D, Hassard L;  
PI Harding J, Charreyre CE, Chappuis GE, Krakowka GS, Audonnet JF;  
PI Mcneilly F;  
XX  
DR WPI: 2001-244408/25.  
DR P-PSDB; AAB73273.  
XX  
PT Use of porcine circovirus-2 immunogen to formulate a vaccine  
PT composition to treat pigs against myocarditis, abortion, intrauterine  
PT infection and/or post-weaning, multisystemic wasting syndrome  
PT associated with PCV-2 -  
XX  
XX Example 3 #3; Fig 6 #1; 134pp; English.  
PS  
XX  
XX The present invention relates to the use of porcine circovirus-2 (PCV-2)  
CC immunogen to formulate a vaccine composition to prevent or treat pigs

CC against myocarditis and/or abortion and/or intrauterine infection and/or  
CC post-weaning, multisystemic wasting syndrome and other pathological  
CC sequelae associated with PCV-2. The present sequence is a DNA fragment of  
CC a plasmid, which expresses gene products of PCV-2.  
XX  
SQ Sequence 2769 BP; 828 A; 455 C; 538 G; 948 T; 0 other;  
  
Query Match 88.6%; Score 622; DB 22; Length 2769;  
Best Local Similarity 92.9%; Pred. No. 8.2e-178;  
Matches 652; Conservative 0; Mismatches 50; Indels 0; Gaps 0;  
  
QY 1 atgcgctatcaaggagcggttacccaagaagaagacaccccccgcagccatcttggc 60  
Db 1898 ATGACGTATCCAAGGAGCGGTTACCGCAGAGAGACACCGCCCGCAGCCATCTTGGC 1839  
QY 61 cagatccctcccccgcgcctcgctgcctccaccccccacccgttacgcgtggaag 120  
Db 1838 CAGATCCCTCCCGCGCGCCCTGCTCGTCCACCCCGCCACCGTACCCTGGAGAGG 1779  
QY 121 aaaaatggcatcttcaacacccgcctctcccgacacttcgggatactgtcaagcaacc 180  
Db 1778 AAAAAATGCACTTCAACACCCGCTCTCCCGCACCTTCGGATATATCTCAAGCGTACC 1719  
QY 181 acagtcagaacgcctcctggggcggtggaacatgatgattcaattaatgactttctt 240  
Db 1718 ACAGTCACACGCGCTCTCGGCGGTGGACATGATGAGATTTAAAAATTCAGCAGCTTTGTT 1659  
QY 241 cccccagaggggggtcaaacccccgcctctgtgccttttgataactacagaataagaag 300  
Db 1658 CCCCCGGAGGGGGGAGCAAAAAATCTCTATACCTTTTGAATATACAGAAATAGAAAG 1599  
QY 301 gtaaggttgaaattctgcctcctcccgatcccccaggtgacaggggtgagggagtgagctcc 360  
Db 1598 GTTAAGGTTGAAATCTGGCCCTGCTCCGCCATCACCCAGGGTGATAGGGGAGTGGGCTCC 1539  
QY 361 agtgcgttatttttagatgataaactttgtacaagaagccacagccctcacctatgacccc 420  
Db 1538 ACTGCTGTTATCTTAGATGATAAATTTGTAAAGAGCCACAGCCCTAACCTATGACCCA 1479  
QY 421 tatgtaaactactctccgcgcatacacaataccacagccctctctaccactcccggtac 480  
Db 1478 TATGTAAACTACTCTCCCGCATACAATCCCCCAACCCCTTCTCTACCCACTCCGCTTAC 1419  
QY 481 ttacccccacacctgtccttagatttcaactattgatacttccacacaaacaaaga 540  
Db 1418 TTCACACCAACACCTGTTCTTGACTCCCACTATGTGATTTACTTCCAAACCAAAATACAAAGG 1359  
QY 541 aaccagctgtggctgagactacaactgtggaattgtagaccacgtagccctcgccact 600  
Db 1358 AATCAGCTTTGGCTGAGACTACAAACCTCTGGAATGTGGACCACTAGGCCCTCGGCGCT 1299  
QY 601 gcgttcgaacacagtatatagaccaggaatacaataatccgtgttaaccatgtatgtacaa 660  
Db 1298 GCGTTCGAAAAACAGTAAATAGCAGCAGACTACAATATCCGTTGTAACCATGTATGTACAA 1239  
QY 661 ttcagagaatttaatttaaagaccccccaacttaacccttaa 702  
Db 1238 TTCAGAGAATTAAATCTTTAAAGACCCCCCACTTAAACCCCTAA 1197  
  
RESULT 4  
AAAF28320/c  
ID AAF28320 standard; DNA; 3609 BP.  
XX  
AC AAF28320;  
XX  
DT 30-MAR-2001 (first entry)  
XX  
DE pJP107 donor plasmid for PCV2 ORF2 and ORF1.  
XX  
KW PCV2; porcine circovirus 2; virucide; immunostimulant; vaccine;  
KW postweaning multisystemic wasting syndrome; PMWS; infection;

KW pig pathogen; open reading frame; ORF; ss.  
XX Porcine circovirus type 2.  
OS Synthetic.  
XX  
XX  
XX  
XX WO200077216-A2.  
XX  
XX 21-DEC-2000.  
XX  
XX 09-JUN-2000; 2000WO-IB00882.  
XX  
XX 10-JUN-1999; 99US-0138478.  
XX 01-JUN-2000; 2000US-0583545.  
XX  
XX (MERT-) MERIAL.  
XX  
XX  
XX Bublot M, Perez JM, Charreyre CE;  
XX  
XX WPI; 2001-080692/09.  
XX P-PSDB; AAB61155, AAB61156.  
XX  
XX Novel recombinant virus comprising DNA from porcine circovirus 2 useful  
XX as vaccine for treatment and prophylaxis of porcine circovirus  
XX infection, such as postweaning multisystemic wasting syndrome in pigs  
XX  
XX  
XX Example 3; Fig 6; 60pp; English.  
XX  
XX The present sequence was used in the construction of a recombinant  
XX virus comprising DNA from porcine circovirus 2 (PCV2). The  
XX recombinant virus is useful as vaccine for treatment and prophylaxis of  
XX PCV2 infection, such as postweaning multisystemic wasting syndrome (PMWS)  
XX in young pigs.  
XX  
XX Sequence 3609 BP; 1050 A; 618 C; 737 G; 1204 T; 0 other;

Query Match 88.6%; Score 622; DB 22; Length 3609;  
Best Local Similarity 92.9%; Pred. No. 9.3e-178;  
Matches 652; Conservative 0; Mismatches 50; Indels 0; Gaps 0;  
  
Qy 1 atgacgtatccaaaggagcgtttaccgaagaagaagacaccccccagccatcttggc 60  
Db 1898 ATACGCTATCCAAAGGAGCGCTTACCGAGAAGAAGACACCGCCCGCAGGCATCTTGGC 1839  
  
Qy 61 cagatctccgcgcgcgcctcgtcgtccaccccccacccgcttaccgctgagaagg 120  
Db 1838 CAGATCTCCGCGCCGCCCTGCTGCTCACCCTCCCGCCCGCTACCGTTGGAGAAGG 1779  
  
Qy 121 aaaaatggcatcttcaacacccgcctctccgcacccctcggatatactgtcaagcgaacc 180  
Db 1778 AAAAATGGCATCTTCAACACCCCGCCTCTCCGCGACCTTCGGATATCTGTCAAGGTACC 1719  
  
Qy 181 acsgtcagaacgcctcctcctcgtggcggtgagacatgatgagattcaataattattttt 240  
Db 1718 ACAGTTCACAACGCGCCTCCTCGGCGGTGACATGATGAGATTAAATTTAGACTTTGTT 1659  
  
Qy 241 cccccggagggggtcaaacccccgcctcgtgccccttgaatactacagaataaagaag 300  
Db 1658 CCCCCGGAGGGGGACCAACAAATCTCTATACCTTTTGAATACTACAGAAATAGAAAG 1599  
  
Qy 301 gttaaagttgaattctggcctcgtcccccgatcacccagggtgacagggggggtggctcc 360  
Db 1598 GTTAAAGTTGAATTCTGGCCCTGCTCCCCCATCACCCAGGGTGATAGGGGAGTGGGCTCC 1539  
  
Qy 361 agtgcgttatttttagatataactttgtaacaaagccacagccctcactatgaccccc 420  
Db 1538 ACTGCCTGTTATTTAGATGATAACTTTGTAAACAAAGGCCACAGCCCTAACCTATGACCCA 1479  
  
Qy 421 tatgtaaaactactcctcccccataaccataaacccagcccttctcctaccactcccggtac 480  
Db 1478 TATGTAAACTACTCCTCCCGCCATACAAATCCCCCAACCCCTTCTCTACCCTCCCGTTAC 1419

Qy 481 tttacccccaaacctgctcctagatttcaactattgatttcaacaaacaaacaaaga 540  
Db 1418 TTCACACCCAAACCTGTTCTTACTCCCACTATTGATTACTTCCAAACAATAACAAAGG 1359  
  
Qy 541 aaccagctggtgctgagactacaactgctgaaaatgtagaccacgtagcctcggcact 600  
Db 1358 AATCAGCTTTGGCTGAGACTCAAACTCTGGAATGTGGACACCTAGCCCTCGCGGCT 1299  
  
Qy 601 gcgttcgaaacagtatatacagaccaggaatacaataatccgtgtaaccatgtatgacaa 660  
Db 1298 GCGTTCGAAACAGTAAATACGACCCAGGACTACAATATCCGTGTACCATGTATGTACAA 1239  
  
Qy 661 ttcagagaatttaattttaagaaccccccaacttaacccttaa 702  
Db 1238 TTCAGAGAATTTAATCTTAAAGACCCCCCACTTAAACCTAA 1197  
  
RESULT 5  
AAX83754/c  
ID AAX83754 standard; DNA; 1768 BP.  
XX  
XX AC AAX83754;  
XX  
XX 27-AUG-1999 (first entry)  
XX  
XX Porcine circovirus type II 412 nucleotide sequence.  
XX  
XX Porcine circovirus type II; PCVII; PCVI; pig; infection; vaccine;  
XX postweaning multisystemic wasting syndrome virus; diagnosis; ds.  
XX  
XX Porcine circovirus.  
XX OS  
XX WO9929717-A2.  
XX  
XX 17-JUN-1999.  
XX  
XX 11-DEC-1998; 98WO-CA01130.  
XX  
XX 16-DEC-1997; 97US-0069750.  
XX 11-DEC-1997; 97US-0069233.  
XX  
XX (UYSA-) UNIV SASKATCHEWAN.  
XX  
XX Babiuk LA, Potter AA, Wang L, Willson P;  
XX WPI; 1999-394957/33.  
XX  
XX New isolated porcine circovirus Type II  
XX  
XX Claim 1; Fig 2; 82pp; English.  
XX  
XX The present invention describes a new isolated porcine circovirus  
XX Type II (PCVII), obtained from postweaning multisystemic wasting  
XX syndrome-affected pigs. AAX83754 to AAX83757 represent PCVII nucleotide  
XX sequences. AAY24929 to AAY24934 represent PCVII open reading frame (ORF)  
XX proteins (N.B. the PCVII ORFs given in Fig 2A to Fig 2B do not  
XX correspond exactly with the PCVII ORFs given in Fig 3A to Fig 3D).  
XX The PCVII polypeptides can be used for treating or preventing PCVII  
XX infection in vertebrates. The products can also be used to detect the  
XX PCVII.  
XX  
XX Sequence 1768 BP; 454 A; 361 C; 492 G; 461 T; 0 other;  
XX  
  
Query Match 88.4%; Score 620.4; DB 20; Length 1768;  
Best Local Similarity 92.7%; Pred. No. 2e-177;  
Matches 651; Conservative 0; Mismatches 51; Indels 0; Gaps 0;  
  
Qy 1 atgacgtatccaaaggcgtttaccgaagaagaagacaccccccagccatcttggc 60  
Db 1735 ATGACGTATCCAAAGGAGCGGTACCGCAGAGAAGACACCGCCCGCAGCCATCTTGGC 1676  
  
Qy 61 cagatcctccgcgcgcctcgtcgtccaccccccgcacccgttaccgcgtggagaagg 120

```
Db 1675 CAGATCTCGCGCGCGCCCTGCTGCTCCACCCCGCCACCGCTACCGTTGGAGAAGG 1616
Qy 121 aaaaatggcatcttcaacaccccgctctcccgccaccccttcggatatactgtcaagcgaa 180
Db 1615 AAAAATGGCATCTTCAACACCCGCTCTCCCGCACCTTCGGATATACTGTCAAGCGTACC 1556
Qy 181 acagtcagaagccctccctcctggcggtggacatgatgagatcgaatattatgactttctt 240
Db 1555 ACAGTCACAAACGCCCTCTCTGGCGGTGGACATGATGAGATTTAAAATTGACGACTTTGTT 1496
Qy 241 ccccgagggggggtcaaaccccgctctgtccctttgaatactacagaataagaag 300
Db 1495 CCCCCGGAGGGGGACCAAAAATCTCTATACCCCTTTGAAATACTACAGAAATAGAAAG 1436
Qy 301 gtttaaggttgaattctggcctctcccgatcacccaggtgacagggagtggtcc 360
Db 1435 GTTAAGGTTGAATCTGCGCTTCTCTCCCCATCACCAGGGTGATAGGGAGTGGGTCC 1376
Qy 361 agtgcgttatttttagatgataaactttgtaacaaagccacagccctacccatgacccc 420
Db 1375 ACTGCTGTTATTTTAGATGATAACTTTGTAACAAAGGCCACAGCCCTTAACCTATGACCCA 1316
Qy 421 tatgtaaactactctcccgcaataccataaaccagcccttctctaccactcccggtac 480
Db 1315 TATGTAAACTACTCTCTCCGCGCATACATCCCCAACCCCTTCTCTACCACTCCCGTTAC 1256
Qy 481 ttacccccaaactctctctagatttcaactattgattacttccaaacaaacaaaga 540
Db 1255 TTCACACCCCAAACTGTTGACTCCACTATTGATTACTTCCACCAATAACAAAGG 1196
Qy 541 aaccagctgggtgagactacaaaactgctggaatgtagaccacgtaggcctcgccact 600
Db 1195 AATCAGCTTTGGGTGAGGCTACAAACCTCTGGAATGTGGACACAGTGGCCTCGGCAC 1136
Qy 601 ggggtcgaaaacagtataacgacagggaataacaataatccgtgtacccatgtatgtacaa 660
Db 1135 GGGTTCGAAACACAGTAATAACGACACAGGACTACAATAATCCGTGTAAACCATGTGTACAA 1076
Qy 661 ttcagagaatttaatttaagaaccccccaacttaaccccttaa 702
Db 1075 TTCAGAGAATTTAATCTTAAGACCCCCCCTTGAACCCCTAA 1034

RESULT 6
AAF75841/c
ID AAF75841 standard; DNA; 1768 BP.
XX AC AAF75841;
XX DT 18-MAY-2001 (first entry)
XX DE PCV DNA fragment of Imp 1121 strain.
XX KW Vaccine; pig; myocarditis; abortion; intrauterine infection;
XX KW multisystemic wasting syndrome; ds.
XX OS Porcine circovirus-2.
XX PN WO200116330-A2.
XX PD 08-MAR-2001.
XX PF 28-AUG-2000; 2000WO-EP08781.
XX PR 31-AUG-1999; 99US-0151564.
XX PR 31-MAY-2000; 2000US-0583350.
XX PA (MERI-) MERIAL.
XX PA (UYSA-) UNIV SASKATCHEWAN.
XX PA (UYBE-) UNIV QUEENS BELFAST.
XX PI Ellis JA, Allan GM, Meehan B, Clark E, Haines D, Hassard L;
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PI Harding J, Charreyre CE, Chappuis GE, Krakowka GS, Audonnet JF;
PI Mcneilly F;
XX WPI; 2001-244408/25.
XX Use of porcine circovirus-2 immunogen to formulate a vaccine
PT composition to treat pigs against myocarditis, abortion, intrauterine
PT infection and/or post-weaning, multisystemic wasting syndrome
PT associated with PCV-2 -
XX Claim 11; Fig 7; 134pp; English.
XX The present invention relates to the use of porcine circovirus-2 (PCV-2)
CC immunogen to formulate a vaccine composition to prevent or treat pigs
CC against myocarditis and/or abortion and/or intrauterine infection and/or
CC post-weaning, multisystemic wasting syndrome and other pathological
CC sequelae associated with PCV-2. The present sequence is a DNA fragment of
CC a strain of PCV, which was used in the present invention.
XX Sequence 1768 BP; 452 A; 359 C; 496 G; 461 T; 0 other;
```

```
Query Match 87.9%; Score 617.2; DB 22; Length 1768;
Best Local Similarity 92.5%; Pred. No. 1.9e-176;
Matches 649; Conservative 0; Mismatches 53; Indels 0; Gaps 0;

Qy 1 atgcgtatccaaagagggcgttacgaaagaagacacccgcccgcgagccatcttggc 60
Db 1735 ATGAGCTATCCAAGGAGCGGTACCGCAGAGAAGACACCGCCCGCAGCCATCTTGGC 1676
Qy 61 cagatctcccgcccgccctggctgtccacccccccacccgttaccgctggagaagg 120
Db 1675 CAGATCTCCCGCGCGCCCTGGCTCTCCACCCCGCCACCGCTACCGTTGGAGAAGG 1616
Qy 121 aaaaatggcatcttcaacaccccgctctcccgcaacttccgatactatgtaagaagacc 180
Db 1615 AAAAATGGCATCTTCAACACCCCGCTCTCCCGCACCTTTCGGATATACTGTCAAGCGTACT 1556
Qy 181 acagtcaagaacgctctctggcggtgacatgatgagatcaattatgaactttctt 240
Db 1555 ACAGTCACACGCCCTCTCTGGCGGTGGACATGATGAGATTTAAAATTGACGACTTTGTT 1496
Qy 241 ccccgaggggggtcaaaccccccgctctgtgcccctttgaaatactacagaataagaag 300
Db 1495 CCCCCGGAGGGGGACCAAAAATCTCTATACCCCTTTGAATACTACAGAAATAGAAAG 1436
Qy 301 gtttaaggttgaattctggcctctcccgatcacccaggtgacagggagtggtcc 360
Db 1435 GTTAAGGTTGAATCTGCGCTTCTCTCCCCATCACCAGGGTGATAGGGAGTGGGTCC 1376
Qy 361 agtgcgttatttttagatgataaactttgtaacaaagccacagccctacccatgacccc 420
Db 1375 ACTGCTGTTATTTTAGATGATAACTTTGTAACAAAGGCCACAGCCCTTAACCTATGACCCA 1316
Qy 421 tatgtaaactactctcccgcaataccataaaccagcccttctctaccactcccggtac 480
Db 1315 TATGTAAACTACTCTCTCCGCGCATACATCCCCAACCCCTTCTCTACCACTCCCGTTAC 1256
Qy 481 ttacccccaaactctctctagatttcaactattgattacttccaaacaaacaaaga 540
Db 1255 TTCACACCCAAACCTGTTCTTGGCTCCACTATTGATTACTTCCAAACCAATAACAAAGG 1196
Qy 541 aaccagctgggtgagactacaaaactgtggaatgtagaccagtaggcctcgccact 600
Db 1195 AATCAGCTTTGGGTGAGGCTACAAACCTCTGGAATGTGGACACAGTGGCCTCGGCAC 1136
Qy 601 ggggtcgaaaacagtataacgacagggaataacaataatccgtgtacccatgtatgtacaa 660
Db 1135 GGGTTCGAAACACAGTAATAACGACACAGGACTACAATAATCCGTGTAAACCATGTGTACAA 1076
Qy 661 ttcagagaatttaatttaagaaccccccaacttaaccccttaa 702
Db 1075 TTCAGAGAATTTAATCTTAAGACCCCCCCTTGAACCCCTAA 1034
```

RESULT	7	
ID	AAF75840/C	
XX	AAF75840 standard; DNA; 1768 BP.	
XX		
AC	AAF75840;	
DT	18-MAY-2001 (first entry)	
XX		
DE	PCV DNA fragment of Imp 1103 strain.	
XX		
KW	Vaccine; pig; myocarditis; abortion; intrauterine infection;	
KW	multisystemic wasting syndrome; ds.	
XX		
OS	Porcine circovirus-2.	
XX		
PN	WO200116330-A2.	
XX		
PD	08-MAR-2001.	
XX		
PF	28-AUG-2000; 2000WO-EP08781.	
XX		
XX	31-AUG-1999; 99US-0151564.	
PR	31-MAY-2000; 2000US-0583350.	
XX		
PA	(MERI-) MERIAL.	
PA	(UYSA-) UNIV SASKATCHEWAN.	
PA	(UYBE-) UNIV QUEENS BELFAST.	
XX		
PI	Ellis JA, Allan GM, Meehan B, Clark E, Haines D, Hassard L;	
PI	Harding J, Charreyre CE, Chappuis GE, Krakowka GS, Audonnet JF;	
PI	Mcneilly F;	
XX		
DR	WPI; 2001-244408/25.	
XX		
PT	Use of porcine circovirus-2 immunogen to formulate a vaccine	
PT	composition to treat pigs against myocarditis, abortion, intrauterine	
PT	infection and/or post-weaning, multisystemic wasting syndrome	
PT	associated with PCV-2	
XX		
PS	Claim 10; Fig 6 #2; 134pp; English.	
XX		
CC	The present invention relates to the use of porcine circovirus-2 (PCV-2)	
CC	immunogen to formulate a vaccine composition to prevent or treat pigs	
CC	against myocarditis and/or abortion and/or intrauterine infection and/or	
CC	post-weaning, multisystemic wasting syndrome and other pathological	
CC	sequelae associated with PCV-2. The present sequence is a DNA fragment of	
CC	a strain of PCV, which was used in the present invention.	
XX		
SQ	Sequence 1768 BP; 450 A; 360 C; 496 G; 460 T; 2 other;	
Query Match	87.2%;	Score 612.4; DB 22; Length 1768;
Best Local Similarity	92.0%;	Pred. No. 5.3e-175;
Matches	646; Conservative	0; Mismatches 56; Indels 0; Gaps 0;
QY	1	atgacatattccaaggaggcgttaccggaagaagaacacgcccccgagccattctggc 60
DB	1735	ATGACATATCCAAGGAGCGCTTACCGCAGAAGAAGACACCGCCCCCGACCATCTTGGC 1676
QY	61	cagatctccgcgcgcgccttgcttcaccccgccaccccgccacccgttaccgctggagaagg 120
DB	1675	CAGATCTCGCGCGCGCCCTCGTCTGCTCCACCCCGCCACCCGCTACCGTGTGGAGAGG 1616
QY	121	aaaaatggcatcttcaacaccccgcttcgcgcacccctccgcatctcgatatactgtcaagcaacc 180
DB	1615	AAAAATGGCATCTTCAACACCCGCCCTCTCCCGCACCTTCGGATATCTGTCAACGGTACC 1556
QY	181	acagtcagaacgcctctctggcggtggacatgatgatgatgaattatgaattcttt 240
DB	1555	ACAGTCACACGCGCCCTCTCGCGGGGTGGACATGATGATGATTAATAATGACGACTTTGTT 1496

Qy	241	ccccccaggagggtgcaaacccccgctctgtgcccctttgaatactactacagaataagaag 300
Db	1495	CCCCCGGAGGGGGACCAAAAATCTCTATACCTTTTGAATACTACAGAATAAGAAAG 1436
Qy	301	gttaaggttgaaattctgcccctgtccccgcatcacccagggtgacaggggagtggtctcc 360
Db	1435	GTTAAGGTGAATTCTGGCCCTGCTCCCCCATCACCCAGGGGTAGAGGGGAGTGGGCTCC 1376
Qy	361	agtgctgttatttagatgataactttgttaacaaaggccacacgcccctcacctatgacccc 420
Db	1375	ACTGCTGTTATTCATAGATGATAAATTTGTACCAAGGCCACAGCCCAACATATGACCCA 1316
Qy	421	tatgtaactactctccgcgcataaccataacccagccctctctacacactcccggtac 480
Db	1315	TATGTAACACTACTCTCCCGCATACAAATCCCCCAACGCTTCTCTACCACTCCCGTTAC 1256
Qy	481	tttacccccaaacctgtctagatttcaactattgtatttacttaccacaaacaaaga 540
Db	1255	TTCACACCCAAACCTGTTCTTGACTCCACTATTGTATTACTTCCAAACCAATAACAAAAGG 1196
Qy	541	aaccagctgtgctgagactcaaaactgctggaatgtagaccagtaggctcggcact 600
Db	1195	AATCAGCTTTGGCTGAGGCTACAAACCTCTAGAAATGTGGACCACGCTAGGCCCTCGCACT 1136
Qy	601	gcgttcgaaaacagtatatacagaccaggaatacaataatccgtgttaaccatgtatgataa 660
Db	1135	CGGTTCGAAAACAGTAAATACGACCAGGACTACAATATCCGTTAACCTGTATGTACAA 1076
Qy	661	ttcagagaaatttaattttaagaccccccaacttaacccttaa 702
Db	1075	TTCAGGGAATTAATCTTAAAGACCCCCCACTTAACCCCTAA 1034

RESULT 8  
AAX83755/C  
ID AAX83755 standard; DNA; 1786 BP.  
XX  
AC AAX83755;  
XX  
DT 27-AUG-1999 (first entry)  
XX  
DE Porcine circovirus type II 9741 nucleotide sequence.  
XX  
KW Porcine circovirus type II; PCVII; PCVI; pig; infection; vaccine;  
KW postweaning multisystemic wasting syndrome virus; diagnosis; ds.  
XX  
OS Porcine circovirus.  
XX  
PN WO9929717-A2.  
XX  
PD 17-JUN-1999.  
XX  
PF 11-DEC-1998; 98WO-CA01130.  
XX  
PR 16-DEC-1997; 97US-0069750.  
PR 11-DEC-1997; 97US-0069233.  
XX  
PA (UYSA-) UNIV SASKATCHEWAN.  
XX  
PI Babiuk LA, Potter AA, Wang L, Willson P;  
XX  
DR WPI; 1999-394957/33.  
XX  
PT New isolated porcine circovirus Type II  
XX  
PS Claim 1; Fig 4; 82pp; English.  
XX  
CC The present invention describes a new isolated porcine circovirus  
CC Type II (PCVII), obtained from postweaning multisystemic wasting  
CC syndrome-affected pigs. AAX83754 to AAX83757 represent PCVII nucleotide  
CC sequences. AAY24929 to AAY24934 represent PCVII open reading frame (ORF)  
CC proteins (N.B. the PCVII ORFs given in Fig 2A to Fig 2B do not  
CC correspond exactly with the PCVII ORFs given in Fig 3A to Fig 3D).



```
QY 534 caaaagaaacagcgtgtgctgagactacaaactgctggaatgttagaccacacgtaggcct 593
      ||||| || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 784 CAAAAGGAATCAGCTTTGGCTGAGGTACAAACCTCTGAAAATGTGGACCACTAGGCCT 725
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 594 cgcactgcgttcgaaacagtatatc-gaccagaataacataatccgtgttaaccatgt 652
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 724 CGGCACCTCGGTTCCGAANACAGTAATATACAGACCAGGACTACAAATATCCGTGTACCATGT 665
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 653 atgtacaattcagagaatttaatttttaagagacccccccacttaacccttaa 702
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 664 ATGTACAATTCAGAGAATTAACTTTAAAGACCCCCCCTTAACCCCTAA 615
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 10
ID AAX35378/c
XX AAX35378 standard; DNA; 1767 BP.
AC AAX35378;
XX
DT 07-JUL-1999 (first entry)
DE Nucleotide sequence of PCV isolate Imp1011-48121.
XX
KW PCV isolate; type II porcine circovirus; PCV; PMWS;
KW porcine multisystemic wasting syndrome; pig; vaccine; ss.
XX
OS Porcine circovirus.
XX
PN WO9918214-A1.
XX
PD 15-APR-1999.
XX
PF 01-OCT-1998; 98WO-FR02107.
XX
PR 20-MAR-1998; 98FR-0003707.
PR 03-OCT-1997; 97FR-0012382.
PR 22-JAN-1998; 98FR-0000873.
XX
XX (MERI-) MERIAL.
PA (UYBE-) UNIV QUEBENS RELEAST.
PA (UYSA-) UNIV SASKATCHEWAN.
XX
XX Allan G, Chappuis GE, Charreyre CE, Clark E, Ellis J;
PI Haines D, Harding J, Hassard L, Meehan B;
XX
XX WPI; 1999-264024/22.
XX
XX New type II porcine circovirus
PT
PS Claim 11; Fig 1; 56pp; French.
XX
XX The present sequence represents the nucleotide sequence of PCV isolate
CC Impl011-48121. The specification describes a preparation of type II
CC porcine circovirus (PCV), which is particularly isolated from a lesion,
CC from a pig with symptoms of PMWS (porcine multisystemic wasting
CC syndrome). PCV (attenuated or inactivated), polypeptides derived from
CC it, and vectors that express these polypeptides are all useful in
CC vaccines, suitable for administration to adult or young pigs, or to
CC pregnant sows (for passive immunization of their offspring). DNA
CC isolated from PCV is used for in vivo or in vitro expression of viral
CC polypeptides, also as probes or primers for diagnosis in usual
CC hybridization or amplification assays. These polypeptides may also be
CC used diagnostically to detect PCV-specific antibodies, while antibodies
CC raised against the polypeptides can be used to detect antigens, in any
CC usual immunoassay format.
XX
XX Sequence 1767 BP; 447 A; 360 C; 502 G; 458 T; 0 other;
SQ
```

Query Match 54.4%; Score 381.6; DB 20; Length 1767;  
Best Local Similarity 99.0%; Pred. No. 4.2e-105;  
Matches 384; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

```
QY 315 ctggccctgctccccgatacccaagggtgacaggggagtgggctccagtgctgttatttt 374
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1767 CTGGCCCTGTCTCCCGCATCACCCAGGGTGACAGGGAGTGGGCTCCAGTGTGTTATTCT 1708
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 375 agatgataacttttgaacaaagccacagccctcacctatgacccctatgtaaacctactc 434
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1707 AGATGATAACTTTGTACAAAGGCCACAGCCCTCACCTATGACCCCTATGTAAACTACTC 1648
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 435 ctccgcgcataccataaaccagcccttctctaccactcccggtacttacccccccaacc 494
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1647 CTCCGCCCATACCATACCCAGCCCTTCTCTACCACTCCCGCTACTTTACCCCAAAACC 1588
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 495 tgtctagatttcaactattgatttacttccaacacaaacaaacaaacagacgtggct 554
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1587 TGTCTAGATTCCACTATTGATTACTTCCAAACCAACAAACAAACAAACAGCTGTGGCT 1528
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 555 gagactacaaactctgaaaatgtagaccacgtaggcctcgctcgcttcgaaaaacag 614
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1527 GAGACTACAAACTCTCGAATGTAGACCAGCTAGGCCCTCGGCACCTGGTTTCGAAACAG 1468
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 615 tatacagaccaggaatacaatatccgtgtaaccatgtatgacaattcagagaaatttaa 674
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1467 TATATACGACCAGGAATACAAATATCCGTGTAAACCATGTATGTACAATTCAGAGAAATTTAA 1408
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 675 ttttaagacccccccacttaacccttaa 702
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1407 TCTTAAAGACCCCCCACTTAACCCCTTAA 1380
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 11
AAX35210/c
ID AAX35210 standard; DNA; 1767 BP.
XX
AC AAX35210;
XX
DT 01-JUL-1999 (first entry)
XX
XX Nucleotide sequence of PCV isolate Imp1011-48121.
XX
XX PCV isolate; type II porcine circovirus; PCV; PMWS;
KW porcine multisystemic wasting syndrome; pig; vaccine; ss.
XX
XX Porcine circovirus.
OS
XX
XX FR2769322-A1.
XX
XX 09-APR-1999.
PD
XX
XX 22-JAN-1998; 98FR-0000873.
PF
XX
XX 03-OCT-1997; 97FR-0012382.
PR
XX
XX (MERI-) MERIAL SAS.
PA
XX Allan G, Chappuis GE, Charreyre CE, Clark E, Ellis J;
PI Haines D, Harding J, Hassard L, Meehan B;
XX
XX WPI; 1999-246948/21.
XX
XX New type II porcine circovirus, used for, e.g. passive immunization
PT of pregnant sows
XX
XX Claim 14; Fig 1; 48pp; French.
PS
XX
XX The present sequence represents the nucleotide sequence of PCV isolate
CC Impl011-48121. The specification describes a preparation of type II
CC porcine circovirus (PCV), which is particularly isolated from a lesion,
CC from a pig with symptoms of PMWS (porcine multisystemic wasting
CC syndrome). PCV (attenuated or inactivated), polypeptides derived from
CC it, and vectors that express these polypeptides are all useful in
CC vaccines, suitable for administration to adult or young pigs, or to
CC pregnant sows (for passive immunization of their offspring). DNA
CC isolated from PCV is used for in vivo or in vitro expression of viral
CC polypeptides, also as probes or primers for diagnosis in usual
CC hybridization or amplification assays. These polypeptides may also be
CC used diagnostically to detect PCV-specific antibodies, while antibodies
CC raised against the polypeptides can be used to detect antigens, in any
CC usual immunoassay format.
XX
XX Sequence 1767 BP; 447 A; 360 C; 502 G; 458 T; 0 other;
```

CC isolated from PCV is used for in vivo or in vitro expression of viral  
CC polypeptides, also as probes or primers for diagnosis in usual  
CC hybridization or amplification assays. These polypeptides may also be  
CC used diagnostically to detect PCV-specific antibodies, while antibodies  
CC raised against the polypeptides can be used to detect antigens, in any  
CC usual immunoassay format.

XX Sequence 1767 BP; 447 A; 360 C; 502 G; 458 T; 0 other;

Query Match 54.4%; Score 381.6; DB 20; Length 1767;  
Best Local Similarity 99.0%; Pred. No. 4.2e-105;  
Matches 384; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 315 ctggccctgtcccccgtacccaggggtgacaggggagtggtccagtgctgtatttt 374  
Db 1767 CTGGCCCTGTCTCCCGATACCCAGGGTGACAGGGGAGTGGGCTCCAGTGTATTCT 1708  
Qy 375 agatgataactttgttaacaaagccacagccctcacctatgacccctatgtaaaactactc 434  
Db 1707 AGATGATAACTTTGTAAACAAGGCCACAGCCCTCACCTATGACCCCTATGTAAACTACTC 1648  
Qy 435 ctccggccatacataaccagccctctctaccactcccggtactttaccccccaacc 494  
Db 1647 CTCCGGCCATACCATAACCCAGCCCTTCTCTACCACTCCCGCTACTTTACCCCAAAACC 1588  
Qy 495 tgcctcagatttcactattgtacttccaaacaaacaaagaaagaaacagctgtggct 554  
Db 1587 TGTCTTAGATTCCACTATTGATTCTTCCAAACCAACAAAGAAACACAGCTGTGGCT 1528  
Qy 555 gagactacaaactgctggaaatgtagaccacgtaggcctgggcactgcgttcgaaaaacag 614  
Db 1527 GAGACTACAAACTGCTGGAATGTAGACCACGTAGGCTCGGCACCTGCTTCGAAAAACAG 1468  
Qy 615 tatatcagaccaggaatacataatccggtgaacccatgtatgtacaattcagagaaatttaa 674  
Db 1467 TATATACGACCGAGGAATACAAATATCCGTGTAAACCATGTATGTACAATTCAGAGAAATTAA 1408  
Qy 675 ttttaagaccccccaacttaacccttaa 702  
Db 1407 TCTTAAAGACCCCCCACTTAACCCCTTAA 1380

RESULT 12  
AAZ56869/C  
ID AAZ56869 standard; DNA; 1767 BP.  
XX  
AC AAZ56869;

XX 25-APR-2000 (first entry)  
DT  
DE DNA sequence of PCV Imp.1011-48121 isolate.

XX Antigen; porcine multisystemic wasting syndrome; PMWS; antiviral;  
KW porcine circovirus; PCV; porcine parvovirus; PPV; vaccination; ds.  
XX Porcine circovirus.

XX WO200001409-A2.

PN 13-JAN-2000.

PD 28-JUN-1999; 99WO-EP04598.

PF 06-JUL-1998; 98PR-0008777.

XX (MERI-) MERIAL.

XX (UYBE-) UNIV QUEENS BELFAST.

XX (UYSA-) UNIV SASKATCHEWAN.

PI Allan GM, Meehan BM, Ellis JA, Krakowka GS, Audonnet JF;

XX WPI; 2000-182091/16.

XX Use of a porcine circovirus antigen and a porcine parvovirus antigen  
PT for vaccination against porcine multisystemic wasting syndrome  
XX  
XX Disclosure; Fig 1; 6lpp; English.

XX The invention provides a novel antigenic preparation directed against  
CC porcine multisystemic wasting syndrome (PMWS) that comprises porcine  
CC circovirus (PCV) antigen and porcine parvovirus (PPV) antigen. The PCV  
CC antigens and PPV antigens can be used for vaccination against PMWS. The  
CC present sequence represents the DNA sequence of PCV Imp.1011-48121  
CC isolate.

XX Sequence 1767 BP; 447 A; 360 C; 502 G; 458 T; 0 other;

Query Match 54.4%; Score 381.6; DB 21; Length 1767;  
Best Local Similarity 99.0%; Pred. No. 4.2e-105;  
Matches 384; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 315 ctggccctgtcccccgtacccaggggtgacaggggagtggtccagtgctgtatttt 374  
Db 1767 CTGGCCCTGTCTCCCGATACCCAGGGTGACAGGGGAGTGGGCTCCAGTGTATTCT 1708  
Qy 375 agatgataactttgttaacaaagccacagccctcacctatgacccctatgtaaaactactc 434  
Db 1707 AGATGATAACTTTGTAAACAAGGCCACAGCCCTCACCTATGACCCCTATGTAAACTACTC 1648  
Qy 435 ctccggccatacataaccagccctctctaccactcccggtactttaccccccaacc 494  
Db 1647 CTCCGGCCATACCATAACCCAGCCCTTCTCTTACCACCTCCCGCTACTTTACCCCAAAACC 1588  
Qy 495 tgcctcagatttcactattgtatttccaaacaaacaaagaaagaaacagctgtggct 554  
Db 1587 TGTCTTAGATTCCACTATTGATTCTTCCAAACCAACAAAGAAACACAGCTGTGGCT 1528  
Qy 555 gagactacaaactgctggaaatgtagaccacgtaggcctgggcactgcgttcgaaaaacag 614  
Db 1527 GAGACTACAAACTGCTGGAATGTAGACCACCTAGGCTCGGCACCTGCTTCGAAAAACAG 1468  
Qy 615 tatatcagaccaggaatacataatccggtgaacccatgtatgtacaattcagagaaatttaa 674  
Db 1467 TATATACGACCGAGGAATACAAATATCCGTGTAAACCATGTATGTACAATTCAGAGAAATTAA 1408  
Qy 675 ttttaagaccccccaacttaacccttaa 702  
Db 1407 TCTTAAAGACCCCCCACTTAACCCCTTAA 1380

RESULT 13  
AAF75835/C  
ID AAF75835 standard; DNA; 1767 BP.

XX AAF75835;

XX 18-MAY-2001 (first entry)

XX PCV DNA fragment of Imp 1011-48121 strain.

XX Vaccine; pig; myocarditis; abortion; intrauterine infection;  
KW multisystemic wasting syndrome; ds.

XX Porcine circovirus-2.

XX WO200116330-A2.

XX 08-MAR-2001.

XX 28-AUG-2000; 2000WO-EP08781.

XX 31-AUG-1999; 99US-0151564.

XX 31-MAY-2000; 2000US-0583350.



PA	(MERI-) MERIAL.	OS	Porcine circovirus.
PA	(UYSA-) UNIV SASKATCHEWAN.	XX	
PA	(UYBE-) UNIV QUEENS BELFAST.	PN	WO9918214-AL.
XX		XX	
PI	Ellis JA, Allan GM, Meehan B, Clark E, Haines D, Hassard L;	PD	
PI	Harding J, Charreyre CE, Chappuis GE, Krakowka GS, Audonnet JF;	XX	15-APR-1999.
PI	Mcneilly F;	XX	
XX		PF	01-OCT-1998; 98WO-FR02107.
DR	WPI; 2001-244408/25.	XX	
XX		PR	20-MAR-1998; 98FR-0003707.
PT	Use of porcine circovirus-2 immunogen to the use of porcine circovirus-2 (PCV-2)	PR	03-OCT-1997; 97FR-0012382.
PT	composition to treat pigs against myocarditis, abortion, intrauterine	PR	22-JAN-1998; 98FR-0000873.
PT	infection and/or post-weaning, multisystemic wasting syndrome	XX	
PT	associated with PCV-2 -	XX	
XX		PA	(MERI-) MERIAL.
XX		PA	(UYBE-) UNIV QUEENS BELFAST.
XX		PA	(UYSA-) UNIV SASKATCHEWAN.
XX		XX	
XX	Disclosure; Fig 1 #2; 134pp; English.	XX	
XX		PI	Allan G, Chappuis GE, Charreyre CE, Clark E, Ellis J;
CC	The present invention relates to the use of porcine circovirus-2 (PCV-2)	PI	Haines D, Harding J, Hassard L, Meehan B;
CC	immunogen to formulate a vaccine composition to prevent or treat pigs	XX	
CC	against myocarditis and/or abortion and/or intrauterine infection and/or	DR	WPI; 1999-264024/22.
CC	post-weaning, multisystemic wasting syndrome and other pathological	XX	
CC	sequelae associated with PCV-2. The present sequence is a DNA fragment of	PT	New type II porcine circovirus
CC	a strain of PCV, which was used in the present invention.	XX	
XX		PS	Claim 11; Fig 2; 56pp; French.
XX		XX	
SQ	Sequence 1767 BP; 447 A; 360 C; 502 G; 458 T; 0 other;	XX	
Query Match 54.4%; Score 381.6; DB 22; Length 1767;		CC	The present sequence represents the nucleotide sequence of PCV isolate
Best Local Similarity 99.0%; Pred. No. 4.2e-105; Indels 0; Gaps 0;		CC	Impl011-48285. The specification describes a preparation of type II
Matches 384; Conservative 0; Mismatches 4; Indels 0; Gaps 0;		CC	porcine circovirus (PCV), which is particularly isolated from a lesion,
QY	315 ctggccctgtcccccgtacccagggtgacaggggagtggtccagtgctgtatttt 374	CC	from a pig with symptoms of PMWS (porcine multisystemic wasting
Db	1767 CTGGCCCTGTCCCGGATCACCCAGGGTGACAGGGGAGTGGGCTCCAGTGTATTCT 1708	CC	syndrome). PCV (attenuated or inactivated), polypeptides derived from
QY	375 agatgataactttgttaacaaaggccacagccctcacctatgacccctatgtaactactc 434	CC	it, and vectors that express these polypeptides are all useful in
Db	1707 AGATGATAACTTTGTAAACAAAGGCCACAGCCCTCACCTATGACCCCTATGTAAACTACTC 1648	CC	CC vaccines, suitable for administration to adult or young pigs, or to
QY	435 ctccgcgcataccacagccctctctctacacccctccagctcccggtactttaccaccaacc 494	CC	CC pregnant sows (for passive immunization of their offspring). DNA
Db	1647 CTCCGGCGCATACCATACCCAGCCCTTCTCTACACCTCCCGCTACTTTACCCCAACCC 1588	CC	isolated from PCV is used for in vivo or in vitro expression of viral
QY	495 tgtcctagatttcactattgtattacttccaaacccaaacaaagaaaccagctgtggct 554	CC	polypeptides, also as probes or primers for diagnosis in usual
Db	1587 TGTCTAGATTCCACTATTGATTACTTCCACCAACCAACAAACAAAGAAATCAGCTGTGGCT 1528	CC	hybridization or amplification assays. These polypeptides may also be
QY	555 gagactacaaactgctggaaatgtagaccagctaggcctcgacctcgcttcgaaaaacag 614	CC	used diagnostically to detect PCV-specific antibodies, while antibodies
Db	1527 GAGACTACAAACTTACTGGAAATGTAGACCACAGCTAGGCGCTCGGCCTCGGTAACACAG 1468	CC	CC raised against the polypeptides can be used to detect antigens, in any
QY	615 tatatacagaccaggaatacaatatccgtgtaaacattgtatgtacaattcagagaatttaa 674	CC	CC usual immunoassay format.
Db	1467 TATATACGACAGGAATACAAATATCCGCTGTAAACCATGTATGTACAAATTCAGAGAAATTTAA 1408	XX	SQ Sequence 1767 BP; 448 A; 359 C; 500 G; 460 T; 0 other;
QY	675 ttttaagaccccccaacttaacccttaa 702		
Db	1407 TCTTAAGACCCCCCACTTAACCCCTTAA 1380		
RESULT 14			
ID	AAX35379/c		
ID	AAX35379 standard; DNA; 1767 BP.		
XX			
AC	AAX35379;		
XX			
XX			
DT	07-JUL-1999 (first entry)		
XX			
DE	Nucleotide sequence of PCV isolate Impl011-48285.		
XX			
KW	PCV isolate; type II porcine circovirus; PCV; PMWS;		
XX	porcine multisystemic wasting syndrome; pig; vaccine; ss.		
XX			

